

Customized FORM PTO-1390		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTORNEY DOCKET NO. P07180US00/BAS
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371			U.S. APPLICATION NO. 097830433
INTERNATIONAL APPLICATION NO. PCT/FR99/02643	INTERNATIONAL FILING DATE 28 October 1999	PRIORITY DATE CLAIMED 30 October 1998	
TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES SPECIFIC OF THE NEISSERIA GENUS...			
APPLICANT(S) FOR DO/EO/US: AUJAME et al.			
Applicant herewith submits to the US Designated/Elected Office (DO/EO/US) the following items and other information:			
<p>X 1. This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.</p> <p><input type="checkbox"/> 2. This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 USC 371.</p> <p>X 3. This express request to begin national examination procedures (35 USC 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 USC 371(b) and PCT Art. 22 and 39(1).</p> <p>X 4. A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.</p> <p>X 5. A copy of the International Application as filed (35 U.S.C. 371 (c)(2))</p> <p><input type="checkbox"/> a. is transmitted herewith (required only if not transmitted by the International Bureau).</p> <p>X b. has been transmitted by the International Bureau.</p> <p><input type="checkbox"/> c. is not required, as the application was filed in the United States Receiving Office (RO/US).</p> <p>X 6. A translation of the International Application into English (35 U.S.C. 371(c)(2)).</p> <p><input type="checkbox"/> 7. Amendments to the claims of the International Appln. under PCT Article 19 (35 USC 371 (c)(3))</p> <p><input type="checkbox"/> a. are transmitted herewith (required only if not transmitted by the International Bureau).</p> <p><input type="checkbox"/> b. have been transmitted by the International Bureau.</p> <p><input type="checkbox"/> c. have not been made; however, the time limit for making such amendments had NOT expired.</p> <p><input type="checkbox"/> d. have not been made and will not be made.</p> <p><input type="checkbox"/> 8. A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).</p> <p><input type="checkbox"/> 9. An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).</p> <p><input type="checkbox"/> 10. A translation of the annexes to the Int'l Prelim. Exam. Report under PCT Article 36 (35 U.S.C. 371(c)(5)).</p> <p>Items 11. to 20. below concern document(s) or information included:</p> <p><input type="checkbox"/> 11. An Information Disclosure Statement under 37 C.F.R. 1.97 and 1.98.</p> <p><input type="checkbox"/> 12. An Assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.</p> <p><input type="checkbox"/> 13. A First preliminary amendment.</p> <p><input type="checkbox"/> 14. A Second or Subsequent preliminary amendment.</p> <p><input type="checkbox"/> 15. A substitute specification.</p> <p><input type="checkbox"/> 16. A change of power of attorney and/or address letter.</p> <p><input type="checkbox"/> 17. A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 & 35 USC 1.821-825.</p> <p><input type="checkbox"/> 18. A second copy of the published international application under 35 USC 154(d)(4).</p> <p><input type="checkbox"/> 19. A second copy of the English translation of the international application under 35 USC 154(d)(4).</p> <p><input type="checkbox"/> 20. Other items or information:</p> <p><input type="checkbox"/></p> <p><input type="checkbox"/></p> <p><input type="checkbox"/> A copy of the Notification of Missing Requirements under 35 U.S.C. 371.</p> <p><input type="checkbox"/> In the event that a petition for extension of time is required to be submitted herewith, and in the event that a separate petition does not accompany this response, applicant hereby petitions under 37 CFR 1.136(a) for an extension of time of as many months as are required to render this submission timely. Any fee is authorized in 17(c).</p>			
Date: April 26, 2001			

U.S. APPLICATION NO. <i>known</i> 09/830433		INTERNATIONAL APPLICATION NO. PCT/FR99/02643		ATTORNEY DOCKET NO. P07180US00/BAS	
X 21. The following fees are submitted:				CALCULATIONS <i>PTO USE ONLY</i>	
X Basic National Fee (37 CFR 1.492 (a) (1)-(5):					
<input type="checkbox"/> Neither Int'l Prelim. Exam. fee nor Int'l Search fee paid to USPTO		\$1000			
X Search Report has been prepared by the EPO or JPO		\$ 860			
<input type="checkbox"/> No Int'l Prelim. Ex. fee paid to USPTO but Int'l Search fee paid to USPTO		\$ 710			
<input type="checkbox"/> International preliminary examination fee paid to USPTO		\$ 690			
<input type="checkbox"/> Int'l Prelim. Ex. fee paid to USPTO & all claims satisfied PCT Art. 33(1)-(4)		\$ 100			
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$ 860.00	
<input type="checkbox"/> Surcharge of \$130 for furnishing the oath or declaration later than from the earliest claimed priority date (37 CFR 1.492(e)).				<input type="checkbox"/> 20 mos. \$ <input type="checkbox"/> 30 mos. +	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total Claims	- 20 =		X \$18 =	\$	
Independent Claims	- 03 =		X \$80 =	\$	
<input type="checkbox"/> Multiple Dependent Claim(s) (if applicable)			+ \$270 =	\$	
TOTAL OF ABOVE CALCULATIONS =				\$ 860.00	
<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.				-	
SUBTOTAL =				\$ 860.00	
<input type="checkbox"/> Processing fee of \$130 for furnishing the English translation later than from the earliest claimed priority date (37 CFR 1.492(f)).				<input type="checkbox"/> 20 mos. \$ <input type="checkbox"/> 30 mos. +	
TOTAL NATIONAL FEE =				\$ 860.00	
<input type="checkbox"/> Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40 per property				+	
TOTAL FEES ENCLOSED =				\$ 860.00	
Amount to be				Refunded	\$
				Charged	\$
X a. A check in the amount of \$ 860.00 to cover the above fees is enclosed.					
<input type="checkbox"/> b. Please charge my Deposit Account No. 12-0555 in the amount of \$ to cover the above fees.					
X c. The Commissioner is hereby authorized to charge any additional fees required or credit overpayment to Deposit Account No. 12-0555.					
<i>Note: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.</i>					
SEND ALL CORRESPONDENCE TO:					
B. Aaron Schulman			SIGNATURE: <i>Douglas E. Jackson</i>		
At the address (below) of CUSTOMER NO. 00881.			NAME: Douglas E. Jackson		
LARSON & TAYLOR, PLC			REG. NO.: 28,518		
1199 NORTH FAIRFAX ST.			PHONE NO.: 703-739-4900		
SUITE 900			Date: April 26, 2001		
ALEXANDRIA, VA 22314					

09330433-001501

5

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re patent application of: AUJAME et al.

Serial No.: 09/830,433

Examiner:

Filed: April 26, 2001

Art Unit:

For: NUCLEIC ACID AND POLYPEPTIDES SPECIFIC
OF THE NEISSERIA GENUS...

Docket No.: P07180US00/BAS

PRELIMINARY AMENDMENT

Honorable Commissioner for Patents

Washington, DC 20231

S I R:

In response to the Notice dated December 6, 2001, please amend the application as follows:

IN THE SPECIFICATION:

After Page 49, please substitute the attached Sequence Listing for any Sequence Listing previously filed in the application.

REMARKS

By this Preliminary Amendment, Applicants are submitting a revised Sequence Listing which overcomes the objections pointed out in the Notice dated December 6, 2001, as well as a copy of the paper sequence in computer readable form.

09/830,433:04501

STATEMENT UNDER 37 CFR § 1.821

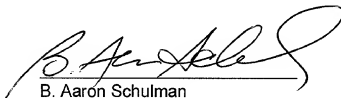
Applicants hereby certify in accordance with 37 C.F.R. 1.821(f) that the content of the enclosed paper sequence listing and computer readable form of the sequence listing are the same. In accordance with 37 C.F.R. 1.821(g), Applicants hereby certify that the enclosed submission contains no new matter.

In light of the foregoing, it is submitted that all prior objections have been overcome, and that the present application should be examined and passed on to allowance at the earliest possible time.

Respectfully submitted,

LARSON & TAYLOR, PLC

Date: February 5, 2002



B. Aaron Schulman
Registration No. 31,877

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent

In re patent application of: AUJAME et al.

Serial No.: 09/830,433

Examiner:

Filed: April 26, 2001

Art Unit:

For: NUCLEIC ACID AND POLYPEPTIDES SPECIFIC
OF THE NEISSERIA GENUS...

Docket No.:

P07180US00/BAS

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C.

S I R:

Prior to examination, please amend the above-identified application as follows.

IN THE SPECIFICATION:

After page 49, please insert the enclosed Sequence Listing as a substitute for the one filed in the original application.

IN THE CLAIMS:

A clean version of the amended claims is provided herewith in **Attachment A**. It will be noted that the claims have been amended relative to the previously provided version as shown by the marked up version thereof in **Attachment B** provided herewith.

REMARKS

By this Amendment, the claims have been rewritten to reduce the multiple dependencies. In addition, in response to the Notice to Comply with the sequence listing requirements, a computer readable form and paper copy of the Sequence Listing is now provided, and Applicants state that the paper copy and computer readable form are identical and add no new matter to the application.

09/830,433-04601

Examination and allowance of the present application is thus earnestly solicited.

Respectfully submitted,

Date: 16 August 2001

By: 
B. Aaron Schulman
Registration No. 31,877

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08830433-054601

ATTACHMENT A

Clean Replacement/New Claims

Following herewith is a clean copy of each claim which replaces each previous claim having the same number and each new claim.

7. (Amended) Expression vector comprising an expression cassette in which a nucleotide sequence as defined in Claim 1 is placed under conditions allowing its expression in a host cell.

9. Canceled.

10. (Amended) Monospecific antibody directed against a polypeptide according to Claim 5.

11. (Amended) Use of a nucleic acid according to Claim 1, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.

12. (New) A pharmaceutical composition comprising a nucleic acid according to Claim 1, in naked form or in combination with at least one agent facilitating transfection, and optionally in combination with a pharmaceutically acceptable vehicle.

13. (New) A pharmaceutical composition comprising a vaccination vector comprising a nucleotide sequence according to Claim 1, such as in particular a virus or a bacterium, and optionally in combination with a pharmaceutically acceptable vehicle.

14. (New) A pharmaceutical composition comprising a polypeptide according to Claim 5, optionally in combination with a pharmaceutically acceptable vehicle.

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ATTACHMENT B

Marked Up Replacement Claims

Following herewith is a marked up copy of each rewritten claim.

7. (Amended) Expression vector comprising an expression cassette in which a nucleotide sequence as defined in ~~one of Claims 1 to 4~~ Claim 1 is placed under conditions allowing its expression in a host cell.

9. Canceled.

10. (Amended) Monospecific antibody directed against a polypeptide according to ~~either of Claims 5 and 6~~ Claim 5.

11. (Amended) Use of a nucleic acid according to ~~one of Claims 1 to 4~~ Claim 1, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, ~~according to either of Claims 5 and 6~~, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.

12. (New) A pharmaceutical composition comprising a nucleic acid according to Claim 1, in naked form or in combination with at least one agent facilitating transfection, and optionally in combination with a pharmaceutically acceptable vehicle.

13. (New) A pharmaceutical composition comprising a vaccination vector comprising a nucleotide sequence according to Claim 1, such as in particular a virus or a bacterium, and optionally in combination with a pharmaceutically acceptable vehicle.

14. (New) A pharmaceutical composition comprising a polypeptide according to Claim 5, optionally in combination with a pharmaceutically acceptable vehicle.

0930433-081631

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09636

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0330373.001601

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His	Ala	Pro	Tyr	Ser	Ala	Leu	Leu	Gln	Pro	Gln	Asp	Lys	Val	Phe	Gly				
						375					380								
Glu	Leu	Ile	Val	Asp	Lys	Tyr	Asp	Asn	Thr	Ile	His	Lys	Thr	Asp	Gln				
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Met	Ile	Gln	Thr	Val	Phe	Glu	Gln	Leu	Gln	Lys	Gln	Pro	Asp	Gly	Asn				
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Trp	Leu	Phe	Ala	Tyr	Thr	Ser	Asp	His	Gly	Gln	Tyr	Val	Arg	Gln	Asp				
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Ile	Tyr	Asn	Gln	Gly	Thr	Val	Gln	Pro	Asp	Ser	Tyr	Leu	Val	Pro	Leu				
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Val	Leu	Tyr	Ser	Ser	Asn	Lys	Ala	Val	Gln	Gln	Ala	Ala	Asn	Gln	Ala				
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Phe	Ala	Pro	Cys	Glu	Ile	Ala	Phe	His	Gln	Gln	Leu	Ser	Thr	Phe	Leu				
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Ile	His	Thr	Leu	Gly	Tyr	Asp	Met	Pro	Val	Ser	Gly	Cys	Arg	Glu	Gly				
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Ser	Val	Thr	Gly	Asn	Leu	Ile	Thr	Gly	Asp	Ala	Gly	Ser	Leu	Asn	Ile				
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 Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly
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 Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Val Ser Tyr Ala
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 Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly
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 Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr
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 Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly
 115 120 125
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 Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser
 130 135 140
 ata tcc ttt ccc gaa ctg tat ggc aga aaa gaa cac ggc tat aac gaa 480
 Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu
 145 150 155 160
 aat tac aaa aac tat acg gcg tat atg cgg aag gaa gcg cct gaa gac 528
 Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp
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 Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile
 180 185 190
 gag act gaa gca aag ccg acg gat atc cgc cac gta aaa gaa atc gga 624
 Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly
 195 200 205
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 His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly
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tca ggc acg ggc ggc ctg atc aaa aaa ggc ggc agc caa ctg caa ctg	500	505	510	1536
Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu				
cac ggc aac aac acc tat acg ggc aaa acc att atc gaa ggc ggt tcg	515	520	525	1584
His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser				
ctg gtg ttg tac ggc aac aaa tcg gat atg cgc gtc gaa acc aaa	530	535	540	1632
Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys				
ggt gcg ctg att tat aac ggc gcg gca tcc ggc ggt agc ctg aac agc	545	550	555	1680
Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser				
gac ggc att gtc tat ctg gca gat acc gac cga tcc ggc gca aac gaa	565	570	575	1728
Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu				
acc gtg cac atc aaa ggc gat ctg cag ctg ggc ggc gaa ggt acg ctg	580	585	590	1776
Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu				
tac aca cgt ttg ggc aaa ctg ctg aaa gtg gac ggt acg gcg atg acc	595	600	605	1824
Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Met Thr				
ggc ggc aag ctg tac atg tcg gca cgc ggc aaa ggc gca ggc tat ctc	610	615	620	1872
Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu				
aac cgt acc gga caa cgt gtt ccc ttc ctg agt gcc gcc aaa atc ggc	625	630	635	1920
Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly				
cgg gat tat tct ttc ttc aca aac atc gaa acc gac ggt ggt ctg ctg	645	650	655	1968
Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu				
gct tcc ctc gac agc gtc gaa aaa aca gcg ggc agt gaa ggc gac acg	660	665	670	2016
Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr				
ctg tcc tat tat gtc cgt cgc ggc aat gcg gca cgg act gct tcg gca	675	680	685	2064
Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala				
gcg gca cat tcc gcg ccc gcc ggt ctg aaa cac gcc gta gaa cag ggc	690	695	700	2112
Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly				
ggc agc aat ctg gaa aac ctg atg gtc gaa ctg gat gcc tcc gaa tca	705	710	715	2160
Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser				
tcc gca aca ccc gag acg gtt gaa act gcg gcc gcc gac cgc aca gat	725	730	735	2208
Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Asp Arg Thr Asp				
atg ccg ggc atc cgc ccc tac ggc gca act ttc cgc gca gcg gca gcc	740	745	750	2256
Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala				

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cgc ctg gtt gcc ggt ctg ggc gcg gat gtc gaa ttc ggc aac ggc tgg 3120
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aac ggc ttg gca cgt tac agc tac gcc ggt tcc aaa cag tac ggc aac 3168
Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn
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50 55 60

Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly
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Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro
85 90 95

Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr
100 105 110

Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly
115 120 125

Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser
130 135 140

Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu
145 150 155 160

Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp
165 170 175

Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile
180 185 190

Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly
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His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly
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Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn
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Thr	His	Asp	Gly	Thr	Lys	Asn	Glu	Ile	Met	Ser	Ala	Ala	Ile	Arg	Asn
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Ala	Trp	Val	Lys	Leu	Gly	Glu	Arg	Gly	Val	Arg	Ile	Val	Asn	Asn	Ser
260				265											
Phe	Gly	Thr	Thr	Ser	Arg	Ala	Gly	Thr	Ala	Asp	His	Phe	Gln	Ile	Ala
275				280											
Asn	Ser	Glu	Glu	Gln	Tyr	Arg	Gln	Ala	Leu	Leu	Ala	Tyr	Ser	Gly	Gly
290				300											
Asp	Lys	Thr	Asp	Glu	Gly	Ile	Arg	Leu	Met	Gln	Gln	Ser	Asp	Tyr	Gly
305				310											
Asn	Leu	Ser	Tyr	His	Ile	Arg	Asn	Lys	Asn	Met	Leu	Phe	Ile	Phe	Ser
325				330											
Ala	Ser	Asn	Asp	Ala	Gln	Ala	Gln	Pro	Asn	Thr	Leu	Thr	Leu	Leu	Pro
340				345											
Phe	Tyr	Glu	Lys	Asp	Ala	Gln	Lys	Gly	Ile	Ile	Thr	Val	Ala	Gly	Val
355				360											
Asp	Arg	Ser	Gly	Glu	Lys	Phe	Asn	Gly	Ser	Asn	His	Cys	Gly	Ile	Thr
370				375											
Ala	Met	Trp	Cys	Leu	Ser	Ala	Pro	Tyr	Glu	Ala	Ser	Val	Arg	Phe	Thr
385				390											
Arg	Thr	Asn	Pro	Ile	Gln	Ile	Ala	Gly	Thr	Ser	Phe	Ser	Ala	Pro	Ile
405				410											
Val	Thr	Gly	Thr	Ala	Ala	Leu	Leu	Leu	Gln	Lys	Tyr	Pro	Trp	Met	Ser
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Asn	Asp	Asn	Leu	Arg	Thr	Thr	Leu	Leu	Thr	Thr	Ala	Gln	Asp	Ile	Gly
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Ala	Val	Gly	Val	Asp	Ser	Lys	Phe	Gly	Trp	Gly	Leu	Leu	Asp	Ala	Gly
450				455											
Lys	Ala	Met	Asn	Gly	Pro	Ala	Ser	Phe	Pro	Phe	Gly	Asp	Phe	Thr	Ala
465				470											
Asp	Thr	Lys	Gly	Thr	Ser	Asp	Ile	Ala	Tyr	Ser	Phe	Arg	Asn	Asp	Ile
485				490											
Ser	Gly	Thr	Gly	Gly	Leu	Ile	Lys	Lys	Gly	Gly	Ser	Gln	Leu	Gln	Leu
500				505											
His	Gly	Asn	Asn	Thr	Tyr	Thr	Gly	Lys	Thr	Ile	Ile	Glu	Gly	Gly	Ser
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Leu	Val	Leu	Tyr	Gly	Asn	Asn	Lys	Ser	Asp	Met	Arg	Val	Glu	Thr	Lys
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Gly	Ala	Leu	Ile	Tyr	Asn	Gly	Ala	Ala	Ser	Gly	Gly	Ser	Leu	Asn	Ser
545				550											
Asp	Gly	Ile	Val	Tyr	Leu	Ala	Asp	Thr	Asp	Arg	Ser	Gly	Ala	Asn	Glu
565				570											
Thr	Val	His	Ile	Lys	Gly	Asp	Leu	Gln	Leu	Gly	Gly	Glu	Gly	Thr	Leu
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Gly	Gly	Lys	Leu	Tyr	Met	Ser	Ala	Arg	Gly	Lys	Gly	Ala	Gly	Tyr	Leu	
		610				615					620					
Asn	Arg	Thr	Gly	Gln	Arg	Val	Pro	Phe	Leu	Ser	Ala	Ala	Lys	Ile	Gly	
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Arg	Asp	Tyr	Ser	Phe	Phe	Thr	Asn	Ile	Glu	Thr	Asp	Gly	Gly	Leu	Leu	
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Ala	Ser	Leu	Asp	Ser	Val	Glu	Lys	Thr	Ala	Gly	Ser	Glu	Gly	Asp	Thr	
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Leu	Ser	Tyr	Tyr	Val	Arg	Arg	Gly	Asn	Ala	Ala	Arg	Thr	Ala	Ser	Ala	
		675					680						685			
Ala	Ala	His	Ser	Ala	Pro	Ala	Gly	Leu	Lys	His	Ala	Val	Glu	Gln	Gly	
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Gly	Ser	Asn	Leu	Glu	Asn	Leu	Met	Val	Glu	Leu	Asp	Ala	Ser	Glu	Ser	
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Ser	Ala	Thr	Pro	Glu	Thr	Val	Glu	Thr	Ala	Ala	Ala	Asp	Arg	Thr	Asp	
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Met	Pro	Gly	Ile	Arg	Pro	Tyr	Gly	Ala	Thr	Phe	Arg	Ala	Ala	Ala	Ala	
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Val	Gln	His	Ala	Asn	Ala	Ala	Asp	Gly	Val	Arg	Ile	Phe	Asn	Ser	Leu	
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Ala	Ala	Thr	Val	Tyr	Ala	Asp	Ser	Thr	Ala	Ala	His	Ala	Asp	Met	Gln	
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Ile	Ala	Ala	Lys	Thr	Gly	Glu	Asn	Thr	Thr	Ala	Ala	Ala	Thr	Leu	Gly	
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		850				855					860					
Ser	Ile	Ser	Leu	Phe	Ala	Gly	Ile	Arg	His	Asp	Ala	Gly	Asp	Ile	Gly	
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Tyr	Leu	Lys	Gly	Leu	Phe	Ser	Tyr	Gly	Arg	Tyr	Lys	Asn	Ser	Ile	Ser	
				885					890					895		
Arg	Ser	Thr	Gly	Ala	Asp	Glu	His	Ala	Glu	Gly	Ser	Val	Asn	Gly	Thr	
			900					905						910		
Leu	Met	Gln	Leu	Gly	Ala	Leu	Gly	Gly	Val	Asn	Val	Pro	Phe	Ala	Ala	
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Thr	Gly	Asp	Leu	Thr	Val	Glu	Gly	Gly	Leu	Arg	Tyr	Asp	Leu	Leu	Lys	
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Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser
965 970 975

Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu
980 985 990

Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly
995 1000 1005

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr
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gca	ggc	tgc	ggc	tca	atc	aat	aat	gta	acc	gtt	tcc	gac	cag	aaa	ctt	96
Ala	Gly	Cys	Gly	Ser	Ile	Asn	Asn	Val	Thr	Val	Ser	Asp	Gln	Lys	Leu	
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Gln	Glu	Arg	Ala	Ala	Phe	Ala	Leu	Gly	Val	Ser	Gln	Asn	Ala	Val	Lys	
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Ile	Ser	Asn	Arg	Ser	Asn	Glu	Ser	Ile	Arg	Ile	Asn	Phe	Thr	Ala	Thr	
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Val	Gly	Lys	Arg	Val	Ser	Gln	Cys	Tyr	Val	Thr	Ser	Val	Ile	Ser	Thr	
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Ile	Gly	Val	Thr	Thr	Ser	Asp	Ala	Ile	Cys	Leu	Gly	Gly	Gly	Thr	His	
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aaa	ggc	aaa	agt	caa	tgc	aat	gct	ttg	ctt	aaa	gcg	gca	ggc	cgt	tgc	336
Lys	Gly	Lys	Ser	Gln	Cys	Asn	Ala	Leu	Leu	Lys	Ala	Ala	Gly	Arg	Cys	
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Leu	Leu	Thr	Glu	Lys	Val	Ser	Pro	Ile	Ile	Ala	Leu	Ile	Leu	Val	Pro			
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Phe	Tyr	Ser	Gly	Gly	Thr	Lys	Ser	Val	Met	Gln	Ile	Val	Ile	Met	Phe			
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Arg	Pro	Met	Ile	Gly	Gly	Leu	Ile	Lys	Leu	Thr	Arg	Gly	Asn	Ile	Val			
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Leu Glu Ala Ala Ser-Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala	
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Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala	
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Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile	
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Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly	
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Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr	
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Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp	
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Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu	
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Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val	
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Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp	
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Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu	

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 Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
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85

90

95

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 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
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Arg	Asp	Ala	Lys	Ser	Ala	Glu	Gly	Ser	Ile	Ser	Ala	Phe	Asn	Asn	Lys	
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Leu	Pro	Leu	Tyr	Arg	Asn	Lys	Ile	Leu	Asn	Leu	Arg	Asp	Val	Glu	Gln	
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Asn	Pro	Leu	Gly	Leu	Ser	Asp	Ser	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly	
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Leu	Val	His	Lys	Thr	Asp	Leu	Thr	Ala	Ala	Thr	Gly	Thr	Glu	Thr	Glu	
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Ser	Gly	Ser	Arg	Ser	Tyr	Ser	Val	His	Tyr	Ser	Val	Pro	Val	Lys	Lys	
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Trp	Leu	Phe	Ser	Phe	Asn	His	Asn	Gly	His	Arg	Tyr	His	Glu	Ala	Thr	
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Ser	Val	Arg	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp	
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Asp	Ala	Glu	Ile	Glu	Val	Gln	Arg	Arg	Arg	Ser	Ala	Gly	Trp	Glu	Ala	
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60

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260 265 270

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Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
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Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
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Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
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Val	Leu	Ile	Gly	Asn	Ala	Gly	Thr	Lys	Pro	Arg	Leu	Ile	Val	Met	His		
		115				120						125					
ctg atg ggt tcg cac agt gat ttt tgc aca cgt ttg gat aag gat gcg 432																	
Leu	Met	Gly	Ser	His	Ser	Asp	Phe	Cys	Thr	Arg	Leu	Asp	Lys	Asp	Ala		
		130				135					140						
cgg cgg ttt cag tat caa act gaa aaa ata tcc tgc tat gtt tcc acc 480																	
Arg	Arg	Phe	Gln	Tyr	Gln	Thr	Glu	Lys	Ile	Ser	Cys	Tyr	Val	Ser	Thr		
	145				150				155						160		
atc gcg caa acc gat aaa ttt tta gaa gat aca gtt aag ata ttg aat 528																	
Ile	Ala	Gln	Thr	Asp	Lys	Phe	Leu	Glu	Asp	Thr	Val	Lys	Ile	Leu	Asn		
				165					170				175				
gaa aat aaa gaa agc tgg tct ttg gtt tac ttt tcc gac cac ggt ttg 576																	
Glu	Asn	Lys	Glu	Ser	Trp	Ser	Leu	Val	Tyr	Phe	Ser	Asp	His	Gly	Leu		
			180					185					190				
atg cat gtc ggt aaa ggc ggc gag cga acg ttg aca cat ggt gcg tgg 624																	
Met	His	Val	Gly	Lys	Gly	Gly	Glu	Arg	Thr	Leu	Thr	His	Gly	Ala	Trp		
		195				200						205					
aag cgt caa agc tac ggc gtg ccg ctg gtt aaa att tcg tcc gat gac 672																	
Lys	Arg	Gln	Ser	Tyr	Gly	Val	Pro	Leu	Val	Lys	Ile	Ser	Ser	Asp	Asp		
		210				215					220						
acg cgg cgc gaa atg att aaa gtg agg cgc agc gcg ttt aat ttt tta 720																	
Thr	Arg	Arg	Glu	Met	Ile	Lys	Val	Arg	Arg	Ser	Ala	Phe	Asn	Phe	Leu		
	225				230					235					240		

Val	Asp	Ala	Arg	Val	Asp	Glu	Asn	Phe	Val	Ile	Met	Ala	Arg	Thr	Asp
145					150					155					160
Ala	Leu	Ala	Val	Glu	Gly	Leu	Asp	Ala	Ala	Ile	Glu	Arg	Ala	Gln	Ala
				165					170					175	
Cys	Val	Glu	Ala	Gly	Ala	Asp	Met	Ile	Phe	Pro	Glu	Ala	Met	Thr	Asp
			180					185					190		
Leu	Asn	Met	Tyr	Arg	Gln	Phe	Ala	Asp	Ala	Val	Lys	Val	Pro	Val	Leu
		195					200					205			
Ala	Asn	Ile	Thr	Glu	Phe	Gly	Ser	Thr	Pro	Leu	Tyr	Thr	Gln	Ser	Glu
		210				215						220			
Leu	Ala	Glu	Asn	Gly	Val	Ser	Leu	Val	Leu	Tyr	Pro	Leu	Ser	Ser	Phe
225				230					235						240
Arg	Ala	Ala	Ser	Lys	Ala	Ala	Leu	Asn	Val	Tyr	Glu	Ala	Ile	Met	Arg
				245					250					255	
Asp	Gly	Thr	Ser	Gly	Gly	Gly	Gly	Gly	Gln	Tyr	Ala	Asn	Pro	Cys	Arg
			260					265					270		
Ala	Val	Arg	Ala	Ser	Glu	Leu	Ser	Cys	Leu	Arg	Ala	Lys	Thr	Gly	
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<211> 921
<212> DNA
<213> Neisseria meningitidis
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<221> CDS  
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Met	Pro	Ser	Ser	Lys	Asn	Trp	Ile	Asn	Cys	Phe	Lys	Asn	Asp	Leu	Pro			
1				5					10					15				
ctt	tca	gac	tgc	ctt	tca	aca	aat	ccg	cat	cgg	tgc	tct	gaa	aac	ccg		96	
Leu	Ser	Asp	Cys	Leu	Ser	Thr	Asn	Pro	His	Arg	Ser	Ser	Glu	Asn	Pro			
			20					25					30					
aaa	ccc	ata	aaa	aca	caa	agg	aga	aat	acc	atg	act	gaa	act	act	caa		144	
Lys	Pro	Ile	Lys	Thr	Gln	Arg	Arg	Asn	Thr	Met	Thr	Glu	Thr	Thr	Gln			
		35					40					45						
acc	ccg	acc	ctc	aaa	cct	aaa	aaa	tcc	gtt	gcg	ctt	tct	ggc	gtt	gcg		192	
Thr	Pro	Thr	Leu	Lys	Pro	Lys	Lys	Ser	Val	Ala	Leu	Ser	Gly	Val	Ala			
	50					55					60							
gcc	ggt	aat	acc	gct	ttg	tgt	acc	gtt	ggc	cgt	acc	ggc	aac	gat	ttg		240	
Ala	Gly	Asn	Thr	Ala	Leu	Cys	Thr	Val	Gly	Arg	Thr	Gly	Asn	Asp	Leu			
65					70					75				80				
agc	tat	cgc	ggt	tac	gac	att	ctg	gat	ttg	gca	caa	aaa	tgt	gag	ttt		288	
Ser	Tyr	Arg	Gly	Tyr	Asp	Ile	Leu	Asp	Leu	Ala	Gln	Lys	Cys	Glu	Phe			
				85					90					95				
gaa	gaa	gtt	gcc	cac	ctg	ctg	att	cac	ggc	cat	tta	ccc	aac	aaa	ttc		336	
Glu	Glu	Val	Ala	His	Leu	Leu	Ile	His	Gly	His	Leu	Pro	Asn	Lys	Phe			
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<210> 38
<211> 306
<212> PRT
<213> Neisseria meningitidis
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Met His Leu Cys Gly Lys Tyr Tyr Gly Val Asn Met Lys Leu Arg Asp	
1 5 10 15	
tta ctg atg gga ata ttc ttg gca gtt tct gcg gcc ctt ctg aat gca	96
Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala	
20 25 30	
acc atc ggc ata ttc agc aag ata ttg atg gag cag gcc ttg tct gtt	144
Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val	
35 40 45	
cag cat att gca ttt ttg aaa act ttg aca ggt ttc gtg ttt atc agc	192
Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser	
50 55 60	
att ttg ctt tgc cgt acc ggt ttt acc aga cag att gcg gat att tca	240
Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser	
65 70 75 80	
aga aag aaa gag gca att ttg ccg ttg ctg tta aaa gta gca att tgt	288
Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Lys Val Ala Ile Cys	
85 90 95	
gct ttt ttc gga att tat acg ttg ttt ttc ttt gaa acc aca gct tat	336
Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr	
100 105 110	
caa tat ggc aat gct gcg aat gta gta gtt gta tta atg gca tcg gct	384
Gln Tyr Gly Asn Ala Ala Asn Val Val Val Leu Met Ala Ser Ala	
115 120 125	
gcc gta tct gcc ttg ata ttg gac agc ata ctg tta gat gaa cgt att	432
Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile	
130 135 140	
tgc att tct tca gtc gtc ggt gtg ggt ttg gca gta ttg ggg atc gca	480
Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala	
145 150 155 160	
atg att tct tgg act gga gaa gga agt tta ggg ttg att ctg aat gcc	528
Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala	
165 170 175	
gca ctg gcg ggc tcg gcc tac ggt tgt ttt tcc gtt ttg att aag aaa	576
Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys	
180 185 190	
ttc ggc cta aac ggc ggt att tat ttg aca cgg ata ttg atg ttt ttt	624
Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe	
195 200 205	
gga agt att ttt ttg ttt atc cct tca ttg gaa ggt att gag gat ata	672
Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile	
210 215 220	
cat tgg caa tgg tct ttt att ccg cca ctc ttg gca ttg tct tta ttg	720
His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu	
225 230 235 240	
ccg acg att tta gga ttt tat tgt aca act aaa gca ttg gat tat ttg	768
Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu	
245 250 255	
agt gct gcg aag gta cag gta act gaa ttg gcc gag cca ttg ttt gct	816
Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala	

0950423.001501

cgc gct acc ttc gcc aat cgc aaa ctg ttt aac gaa atg gtg aaa aac Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn 690 695 700	2112
gaa gac ggc agc gtg cgc caa ggc tgc ttc gcc cgc gtc gaa ccc gaa Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu 705 710 715 720	2160
ggc gaa acc atg cgc atg tgg gaa gcc atc gaa acc tat atg aac cgc Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg 725 730 735	2208
aaa cag cgc ctc atc atc att gcc ggt cgc gac tat ggt caa ggc tca Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser 740 745 750	2256
agc cgc gac tgg gct gca aaa ggc gta cgc ctc gcc ggc gta gaa gcg Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala 755 760 765	2304
att gtt gcc gaa ggc ttc gag cgt atc cac cgc acc aac ctt atc ggc Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly 770 775 780	2352
atg ggc gtg ttg cgc ctg cag ttc aaa ccc gac acc aac cgc cat acc Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr 785 790 795 800	2400
ctg caa ctg gac ggt acg gaa acc tac gac gtg gtc ggc gaa cgc aca Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr 805 810 815	2448
cgc cgc tgc gac ctg acc ctc gtg att cac cgt aaa aac ggc gaa acc Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr 820 825 830	2496
gtc gaa gtt ccc gtt acc tgc cgc ctc gat act gca gaa gaa gta ttg Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu 835 840 845	2544
gta tat gaa gcc ggc ggc gtg ttg caa cgg ttt gca cag gat ttt ttg Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu 850 855 860	2592
gaa ggg aac gcg gct tag Glu Gly Asn Ala Ala 865	2610

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<211> 869

<212> PRT

<213> Neisseria meningitidis

<400> 42

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Glu	Tyr	Tyr	Asp	Ala	Arg	Ala	Ala	Cys	Glu	Asp	Ile	Lys	Pro	Gly	Ser
			20					25					30		

Tyr	Asp	Lys	Leu	Pro	Tyr	Thr	Ser	Arg	Ile	Leu	Ala	Glu	Asn	Leu	Val
		35					40					45			

Asn	Arg	Ala	Asp	Lys	Val	Asp	Leu	Pro	Thr	Leu	Gln	Ser	Trp	Leu	Gly
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09330473.001601

50

55

60

Gln 65	Leu	Ile	Glu	Gly	Lys 70	Gln	Glu	Ile	Asp	Phe 75	Pro	Trp	Tyr	Pro	Ala 80
Arg	Val	Val	Cys	His 85	Asp	Ile	Leu	Gly	Gln 90	Thr	Ala	Leu	Val	Asp 95	Leu
Ala	Gly	Leu	Arg 100	Asp	Ala	Ile	Ala	Glu 105	Lys	Gly	Gly	Asp 110	Pro	Ala	Lys
Val	Asn	Pro	Val	Val	Ala	Lys	Pro	Ser	Phe	Ile	Val	Asp 125	His	Ser	Leu
Ala	Val 130	Glu	Cys	Gly	Gly	Tyr 135	Asp	Pro	Asp	Ala	Phe 140	Arg	Lys	Asn	Arg
Gln 145	Ile	Glu	Asp	Arg	Arg 150	Asn	Glu	Asp	Arg	Phe 155	His	Phe	Ile	Asn	Trp
Thr	Lys	Thr	Ala	Phe 165	Glu	Asn	Val	Asp	Val 170	Ile	Pro	Ala	Gly	Asn 175	Gly
Ile	Met	His	Gln 180	Ile	Asn	Leu	Glu	Lys 185	Met	Ser	Pro	Val	Val 190	Gln	Val
Lys	Asn	Gly 195	Val	Ala	Phe	Pro	Asp 200	Thr	Cys	Val	Gly	Thr 205	Asp	Ser	His
Thr	Pro 210	His	Val	Asp	Ala	Leu 215	Gly	Val	Ile	Ser 220	Val	Gly	Val	Gly	Gly
Leu 225	Glu	Ala	Glu	Thr	Val 230	Met	Leu	Gly	Arg	Ala 235	Ser	Met	Met	Arg	Leu
Pro	Asp	Ile	Val	Gly 245	Val	Glu	Leu	Asn	Gly 250	Lys	Arg	Gln	Ala	Gly 255	Ile
Thr	Ala	Thr	Asp 260	Ile	Val	Leu	Ala	Leu 265	Thr	Glu	Phe	Leu	Arg 270	Lys	Glu
Arg	Val	Val	Gly 275	Ala	Phe	Val	Glu 280	Phe	Phe	Gly	Glu	Gly 285	Ala	Arg	Ser
Leu	Ser 290	Ile	Gly	Asp	Arg	Ala 295	Thr	Ile	Ser	Asn	Met 300	Thr	Pro	Glu	Phe
Gly 305	Ala	Thr	Ala	Ala	Met 310	Phe	Ala	Ile	Asp	Glu 315	Gln	Thr	Ile	Asp	Tyr
Leu	Lys	Leu	Thr	Gly 325	Arg	Asp	Asp	Ala	Gln 330	Val	Lys	Leu	Val	Glu 335	Thr
Tyr	Ala	Lys	Thr 340	Ala	Gly	Leu	Trp	Ala 345	Asp	Ala	Leu	Lys	Thr 350	Ala	Val
Tyr	Pro	Arg 355	Val	Leu	Lys	Phe	Asp 360	Leu	Ser	Ser	Val	Thr 365	Arg	Asn	Met
Ala	Gly 370	Pro	Ser	Asn	Pro	His 375	Ala	Arg	Phe	Ala	Thr 380	Ala	Asp	Leu	Ala
Ser 385	Lys	Gly	Leu	Ala	Lys 390	Pro	Tyr	Glu	Glu	Pro 395	Ser	Asp	Gly	Gln	Met
Pro	Asp	Gly	Ala	Val	Ile	Ile	Ala	Ala	Ile	Thr	Ser	Cys	Thr	Asn	Thr

[illegible]

030309-1

755 760 765

Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly
770 775 780

Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr
785 790 795 800

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr
805 810 815

Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr
820 825 830

Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu
835 840 845

Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu
850 855 860

Glu Gly Asn Ala Ala
865

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<212> DNA
<213> Neisseria meningitidis

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1 5 10 15

aaa ggc gtg ttt ttc aaa cgt tcc gac ctg ccc gag cgc gcg cgg gaa 96
Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
20 25 30

gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc cgg 144
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
35 40 45

gac ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agt tgc tcc 192
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 55 60

acc agc aaa gcc gtg att ttg gac aag tcc gaa cgc acc gat cac gat 240
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
65 70 75 80

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
85 90 95

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110

atc gag caa ggc ttg gtc gat aaa tcc aaa atc cct tca gac gcc cgg 384
Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro
115 120 125

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Pro Glu Asp Cys Phe
385

<210> 44
<211> 389
<212> PRT
<213> *Neisseria meningitidis*

<400> 44
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Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
20 25 30
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
35 40 45
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 55 60
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
65 70 75 80
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
85 90 95
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110
Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro
115 120 125
Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
130 135 140
His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
145 150 155 160
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
165 170 175
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val
180 185 190
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile
195 200 205
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr
210 215 220
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu
225 230 235 240
Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
245 250 255
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
260 265 270
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
275 280 285
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
290 295 300

083043.04604

Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
 85 90 95
 Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu
 100 105 110
 Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His
 115 120 125
 Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln
 130 135 140
 Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala
 145 150 155 160
 Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr
 165 170 175
 Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys
 180 185 190
 Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala
 195 200 205
 Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala
 210 215 220
 Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His
 225 230 235 240
 Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly
 245 250 255
 Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile
 260 265 270
 Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly
 275 280 285
 Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln
 290 295 300
 Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln
 305 310 315

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 <211> 648
 <212> DNA
 <213> Neisseria meningitidis
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 ctg aat gcg cct tcc gaa ctg ggc aaa cag caa aag ttg tgg gcg ttt 96
 Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe
 20 25 30

CCDC131.DAT

Leu Ala Asp Glu Leu Gln Tyr Val Trp Glu His Thr Ala Val Thr Asp
 65 70 75 80
 His Gln Gly Lys Leu Val Glu Ile Pro Val Cys Tyr Gly Gly Glu Tyr
 85 90 95
 Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser
 100 105 110
 Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met
 115 120 125
 Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu
 130 135 140
 His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser
 145 150 155 160
 Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro
 165 170 175
 Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
 180 185 190
 Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
 195 200 205
 Val Ala Glu Arg Ile Glu Pro
 210 215

<210> 49
 <211> 930
 <212> DNA
 <213> Neisseria meningitidis
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 <222> (1)..(927)

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 gga cgc tac gga cac cgg cgt tac ggc atc ggt cat gcc ggt gcg atg 96
 Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
 20 25 30
 gac acg gtt gct ttg gcg gcg ggt aat att tta ttg gcc aac gac gaa 144
 Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu
 35 40 45
 ggc acg gcc gca atc gaa atc gct ttg ggc ggg ata atg ctg gtg ttt 192
 Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
 50 55 60
 gaa cgg gat acg ccg ttt tgt etc acc ggt gcc gtg tat cag gcg gaa 240
 Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
 65 70 75 80
 ttg gac ggc gaa ccg gtc tat tcg tat tgg cgt tat acc gcc cgc aaa 288
 Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
 85 90 95

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[illegible]

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400> 51																	
atg	aat	tcg	acc	gca	agt	aaa	acc	ctg	aaa	gga	ttg	tcg	ctg	gtg	ttt	48	
Met	Asn	Ser	Thr	Ala	Ser	Lys	Thr	Leu	Lys	Gly	Leu	Ser	Leu	Val	Phe		
1				5					10					15			
ttc	gcc	tct	gga	ttc	tgc	gcc	ctg	att	tac	cag	gtc	agc	tgg	cag	agg	96	
Phe	Ala	Ser	Gly	Phe	Cys	Ala	Leu	Ile	Tyr	Gln	Val	Ser	Trp	Gln	Arg		
			20					25					30				
ctt	cta	ttc	agt	cac	ata	ggc	atc	gat	ttg	agt	tcg	att	act	gtc	att	144	
Leu	Leu	Phe	Ser	His	Ile	Gly	Ile	Asp	Leu	Ser	Ser	Ile	Thr	Val	Ile		
			35				40					45					
att	tct	gta	ttt	atg	gtc	ggc	ttg	ggc	gta	ggc	gcg	tat	ttc	ggc	gga	192	
Ile	Ser	Val	Phe	Met	Val	Gly	Leu	Gly	Val	Gly	Ala	Tyr	Phe	Gly	Gly		
	50					55					60						
cgc	att	gct	gac	cgt	ttt	cct	tca	agt	atc	atc	ccc	ctg	ttt	tgc	atc	240	
Arg	Ile	Ala	Asp	Arg	Phe	Pro	Ser	Ser	Ile	Ile	Pro	Leu	Phe	Cys	Ile		
	65				70					75				80			
gct	gaa	gta	tcc	atc	ggc	ctg	ttc	ggc	ttg	gta	agc	agg	ggc	ctg	att	288	
Ala	Glu	Val	Ser	Ile	Gly	Leu	Phe	Gly	Leu	Val	Ser	Arg	Gly	Leu	Ile		
				85					90					95			
tcc	ggc	ttg	ggg	cat	ctt	tta	ggt	gag	gct	gat	ttg	ccc	atc	atc	gct	336	
Ser	Gly	Leu	Gly	His	Leu	Leu	Val	Glu	Ala	Asp	Leu	Pro	Ile	Ile	Ala		
			100					105					110				
gct	gcc	aat	ttc	ctc	tta	ttg	ctg	ctt	cct	acc	ttt	atg	atg	ggc	gcg	384	
Ala	Ala	Asn	Phe	Leu	Leu	Leu	Leu	Leu	Pro	Thr	Phe	Met	Met	Gly	Ala		
			115				120					125					
acc	ttg	ccc	ttg	ctg	acc	tgt	ttt	ttt	aac	cgg	aaa	ata	cat	aat	gtt	432	
Thr	Leu	Pro	Leu	Leu	Thr	Cys	Phe	Phe	Asn	Arg	Lys	Ile	His	Asn	Val		
			130			135					140						
gcy	gag	tct	atc	ggc	ttt	tta	tat	ttt	ttc	aac	ttg	ggc	gcg	gca		480	
Gly	Glu	Ser	Ile	Gly	Thr	Leu	Tyr	Phe	Phe	Asn	Thr	Leu	Gly	Ala	Ala		
	145				150					155				160			
ctc	gga	tcg	ctt	gcc	gcc	gcc	gaa	ttt	ttc	tac	gtc	ttt	ttt	acc	ctc	528	
Leu	Gly	Ser	Leu	Ala	Ala	Ala	Glu	Phe	Phe	Tyr	Val	Phe	Phe	Thr	Leu		
				165				170						175			
tcc	caa	acc	att	gcg	ctg	aca	gcc	tgc	ttt	aac	ctt	ctg	att	gct	gct	576	
Ser	Gln	Thr	Ile	Ala	Leu	Thr	Ala	Cys	Phe	Asn	Leu	Leu	Ile	Ala	Ala		
			180					185					190				
tca	gta	tgc	tgc	gtt	aca	gaa	agg	atg	gat	ata	gtg	aac	act	aaa	cgc	624	
Ser	Val	Cys	Cys	Val	Thr	Glu	Arg	Met	Asp	Ile	Val						

aat Ile	cag Asn	gca Pro	tcc Ala	cgt Tyr	agc Arg	ctt Ser	atc Leu	gcg Ile	gac Ala	gag Asp	ccg Glu	caa Pro	atc Gln	gcc Ile	1584	
ccg Pro	ctt Leu	ttg Leu	cag Gln	gac Asp	aaa Lys	cgt Arg	gtt Val	gaa Glu	att Ile	gta Val	ttg Leu	gat Asp	gac Asp	ggg Gly	agg Arg	1632
aaa Lys	ttg Trp	ctg Leu	cgt Arg	cgc Arg	cat His	cct Pro	gat Asp	gaa Glu	aaa Lys	ttc Phe	gac Asp	ctg Leu	att Ile	ttg Leu	atg Met	1680
aat Asn	acg Thr	act Thr	tgg Trp	tac Tyr	tgg Trp	cgt Arg	gcc Ala	tat Tyr	tcc Ser	acc Thr	aac Asn	ctg Leu	ttg Leu	agt Ser	gcg Ala	1728
gaa Glu	ttt Phe	tta Leu	aaa Lys	cag Gln	gtg Val	caa Gln	agc Ser	cac His	ctt Leu	acc Thr	ccg Pro	gat Asp	ggg Gly	att Ile	gta Val	1776
atg Met	ttt Phe	aat Asn	acc Thr	acg Thr	cac His	agc Ser	ccg Pro	cat His	gct Ala	ttt Phe	gct Ala	acc Thr	gcc Ala	gta Val	cac His	1824
agt Ser	att Ile	ccc Pro	tat Tyr	gca Ala	tac Tyr	cgc Arg	tat Tyr	ggg Gly	cat His	atg Met	gta Val	gtc Val	ggc Gly	tcg Ser	gca Ala	1872
acc Thr	ccg Pro	gta Val	gtt Val	ttc Phe	cct Pro	aat Asn	aaa Lys	gaa Glu	ctg Leu	ctc Leu	aag Lys	caa Gln	cgt Arg	ctc Leu	tcc Ser	1920
cgg Arg	ttg Leu	att Ile	tgg Trp	cgg Pro	gaa Glu	agc Ser	ggc Gly	agg Arg	cac His	gta Val	ttt Phe	gac Asp	agc Ser	agc Ser	acc Thr	1968
gtg Val	gat Asp	gct Ala	gca Ala	gca Ala	caa Gln	aag Lys	gtt Val	gtc Val	tct Ser	cgt Arg	atg Met	ctg Leu	att Ile	cag Gln	atg Met	2016
acg Thr	gaa Glu	cct Pro	tcg Ser	gct Ala	ggg Gly	gcg Ala	gaa Glu	gtc Val	att Ile	acc Thr	gac Asp	gat Asp	aat Asn	atg Met	att Ile	2064
gta Val	gaa Glu	tac Tyr	aaa Lys	tac Tyr	ggc Gly	aga Arg	ggg Gly	att Ile	taa							2094

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<213> Neisseria meningitidis
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Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
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 85 90 95
 Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala
 100 105 110
 Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala
 115 120 125
 Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
 130 135 140
 Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala
 145 150 155 160
 Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu
 165 170 175
 Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala
 180 185 190
 Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro
 195 200 205
 Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser
 210 215 220
 Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln
 225 230 235 240
 Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly
 245 250 255
 Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe
 260 265 270
 Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala
 275 280 285
 Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly
 290 295 300
 Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg
 305 310 315 320
 Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys
 325 330 335
 Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser
 340 345 350
 Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser
 355 360 365
 Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro
 370 375 380
 Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser
 385 390 395 400
 Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp
 405 410 415

0030437.001601

Arg Ala Ala Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg
725 730 735

Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala
740 745 750

His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu
755 760 765

Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp
770 775 780

Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser
785 790 795 800

Thr Gln Thr Val Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala
805 810 815

Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala
820 825 830

Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp
835 840 845

Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr
850 855 860

Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly
865 870 875 880

Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn
885 890 895

Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg
900 905 910

Tyr Asp Leu Leu Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu
915 920 925

Gly Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala
930 935 940

Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala
945 950 955 960

Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr
965 970 975

Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg
980 985 990

Asn Met Pro His Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu
995 1000 1005

Phe Gly Asn Gly Trp Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser
1010 1015 1020

Lys Gln Tyr Gly Asn His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
1025 1030 1035 1040

[illegible]

400> 54																	
atg tct gaa gaa aaa ttg aaa atg agt ttc gag cca acc gta atc gaa																	48
Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu																	
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10																	
15																	
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Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr 768
 225 230 235 240

agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag 768
 Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys 255
 245 250

aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat 816
 Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn 270
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atg ccc gag ttt ttc act gat agc gaa tcc agc cat ttc taa 858
 Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe 285
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 <213> Neisseria gonorrhoeae

<400> 55
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His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu
 20 25 30

Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
 35 40 45

Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
 50 55 60

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg
 65 70 75 80

Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr
 85 90 95

Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys
 100 105 110

Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu
 115 120 125

Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe
 130 135 140

Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr
 145 150 155 160

Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val
 165 170 175

Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile
 180 185 190

Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu
 195 200 205

Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
 210 215 220

Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
 225 230 235 240

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agc ttc ggt tat ttt gtc ggg cgc gtg ttg ccg tat cag ttg ttt gat	576
Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp	
180 185 190	
tta agc aag atc cct gtg ttc aaa cag cct gct cca agc aaa atc ggg	624
Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly	
195 200 205	
caa ggc agt att caa aat atc gtc ctg att atg ggc gaa agc gaa agc	672
Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser	
210 215 220	
gcg gcg cat ttg aaa ttg ttt ggt tac ggg cgc gaa act tcg ccg ttt	720
Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe	
225 230 235 240	
tta acc cgg ctg tcg caa gcc gat ttt aag ccg att gtg aaa caa agt	768
Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser	
245 250 255	
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Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn	
260 265 270	
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Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr	
275 280 285	
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Asn Met. Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr	
290 295 300	
agt gcc cag gct gaa aac caa atg gca att ttg aac tta atc ggt aag	960
Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys	
305 310 315 320	
aaa tgg ata gac cat ctg att cag ccg acg caa ctt ggc tac ggc aac	1008
Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn	
325 330 335	
ggc gac aat atg ccc gat gag aag ctg ctg ccg ttg ttc gac aaa atc	1056
Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile	
340 345 350	
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Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser	
355 360 365	
cac gcc cca tac ggc gca ttg ttg cag cct caa gat aaa gta ttc ggc	1152
His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Asp Lys Val Phe Gly	
370 375 380	
gaa gcc gat att gtg gat aag tac gac aac acc atc cac aaa acc gac	1200
Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp	
385 390 395 400	
caa atg att caa acc gta ttc gag cag ctg caa aag cag cct gac ggc	1248
Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly	
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aac tgg ctg ttt gcc tat acc tcc gat cat ggc cag tat gtg cgc caa	1296
Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln	
420 425 430	
gat atc tac aat caa ggc acg gtg cag ccc gac agc tat att gtg cct	1344
Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro	

435

440

445

ctg gtt ttg tac agc cgc gat aag gcc gtg caa cag gct gcc aac cag 1392
Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln
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Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe
465 470 475 480

ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa 1488
Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu
485 490 495

ggc tgc gta aca ggc aac ctg att acg ggc gat gca ggc agc ttg aac 1536
Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn
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<212> PRT

<213> *Neisseria gonorrhoeae*

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Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala
35 40 45

Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val
50 55 60

Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr
65 70 75 80

Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val
85 90 95

Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu
100 105 110

Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala
115 120 125

Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe
130 135 140

Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His
145 150 155 160

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe
165 170 175

Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp
180 185 190

Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly

100

195

200

205

Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser
210 215 220

Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe
225 230 235 240

Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser
245 250 255

Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn
260 265 270

Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr
275 280 285

Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr
290 295 300

Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys
305 310 315 320

Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn
325 330 335

Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile
340 345 350

Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser
- 355 360 365

His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly
370 375 380

Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp
385 390 395 400

Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly
 405 410 415

Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln
420 425 430

Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro
435 440 445

Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln
450 455 460

Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe
465 470 475 480

Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu
485 490 495

Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn
500 505 510

Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln
515 520

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 Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro
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230

235

240

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260 265 270

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Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
275 280 285

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305 310 315 320

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Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
325 330 335

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<213> *Neisseria gonorrhoeae*

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180 185 190															
Ser	Leu	Phe	Leu	Gly	Val	Arg	Glu	Lys	Arg	Arg	Ile	Val	Arg	Glu	Leu
195 200 205															
Gly	Ala	Leu	Pro	Ala	Val	Ala	Asp	Leu	Ile	Lys	Pro	Ala	Pro	Leu	Ser
210 215 220															
Glu	Glu	Glu	Gln	Lys	Leu	Ala	Arg	Pro	Lys	Leu	Phe	Trp	Trp	Asn	Val
225 230 235 240															
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Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
65 70 75 80
ggg aca att aca gcg aaa ttc gtg gaa gat gga gaa aag gtt aag gct 288
Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala
85 90 95
ggc gac aag cta ttt gcg ctt tgc acc tca cgt ttc gcc gca gga gat 336
Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
100 105 110
agc gtg cag cag cag ttg aaa acg gag gca gtt ttg aag aaa acg ttg 384
Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
115 120 125
gca gaa cag gaa ctg ggt cgt ctg aag ctg ata cac ggg aat gaa acg 432
Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
130 135 140
cgc agc ctt aaa gca act gtc gaa cgt ttg gaa aac cag gaa ctc cat 480
Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Glu Leu His
145 150 155 160
att tgc caa cag ata gac ggt cag aaa agg cgc att aga ctt gcg gaa 528
Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
165 170 175
gaa atg ttg cag aaa tat cgt ttc cta tcc gcc aat gat gca gtg cca 576
Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
180 185 190
aaa caa gaa atg atg aat gtc aag gca gag ctt tta gag cag aaa gcc 624
Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala

SECRET

<222> (1) . . (687)

atg atg aat gtc gag gca gag ctt tta gag cag aaa gcc aaa ctt gat 48
Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp
1 5 10 15

gcc tac ggc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag 96
Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
20 25 30

aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc 144
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
35 40 45

cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt 192
Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
50 55 60

gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcg ggt tat ata 240
Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
65 70 75 80

gca ata ccg aac gtc gaa gtc gga cgg cag gtt gat cct tcc aaa ctg 288
Ala Ile..Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu
- 85 90 95

ctc ttg agc att gtt ccc gaa cgt acc gag tta tat gcc cat cta tat 336
Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
100 105 110

atc ccc agc agt gca gca ggc ttt atc aag ccg aaa gac aag gtt gtc 384
Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
115 120 125

cta cgt tat cag gca tat ccc tat cag aaa ttc ggg ctt gct tcc ggc 432
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
130 135 140

agt gtc gta tca gtg gca aaa acg gca ctg ggc aga cag gaa ttg tcg 480
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
145 150 155 160

gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt 528
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
165 170 175

tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt 576
Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
180 185 190

gag gaa aaa ccg ctg caa atc ggc atg acg ctg gaa gca gac atc cta 624
Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
195 200 205

cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag cgg att tac agt 672
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser
 210 215 220

atg tcg ggc agg ttg taa 69
Met Ser Gly Arg Leu

<210> 65
 <211> 229
 <212> PRT
 <213> *Neisseria gonorrhoeae*

<400> 65
 Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp
 1 5 10 15
 Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
 20 25 30
 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
 35 40 45
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
 50 55 60
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
 65 70 75 80
 Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu
 85 90 95
 Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
 100 105 110
 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
 115 120 125
 Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
 130 135 140
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
 145 150 155 160
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
 165 170 175
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
 180 185 190
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
 195 200 205
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser
 210 215 220
 Met Ser Gly Arg Leu
 225

<210> 66
 <211> 924
 <212> DNA
 <213> *Neisseria gonorrhoeae*

<220>
 <221> CDS
 <222> (1)..(921)

<400> 66

gat gtt gta gaa gtt gcc ccc tct tac gac caa tcc gac att acc gct 864
 Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
 275 280 285

ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg 912
 Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
 290 295 300

aaa aag gac tga 924
 Lys Lys Asp
 305

<210> 67

<211> 307

<212> PRT

<213> Neisseria gonorrhoeae

<400> 67

Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser
 1 5 10 15

Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
 20 25 30

Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
 35 40 45

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
 50 55 60

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
 65 70 75 80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
 85 90 95

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
 100 105 110

Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
 115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
 145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
 180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
 225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
245 250 255

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
290 295 300

Lys Lys Asp
305

<210> 68
<211> 1404
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(1401)

<400> 68
atg aca ttg ctc aat cta atg ata atg caa gat tac ggt att tcc gtt 48
Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
1 5 10 15

tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg 96
Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
20 25 30

aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144
Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
35 40 45

cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca 192
Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
50 55 60

tgg cgg gcg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac 240
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
65 70 75 80

cag cgt gat gca gtg cgc gca cgg caa caa caa gcc aag gcc gca ttc 288
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Ala Lys Ala Ala Phe
85 90 95

ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag ccg cca tcg 336
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
100 105 110

att tct tcc acc cgc gaa aca cag gga tgg agc gtg cag gtg gga caa 384
Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
115 120 125

acc tta ttt gac gct gcc aaa ttt gca caa tac cgc caa agc agg ttc 432
Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
130 135 140

gat acg cag gct gca gaa cag cgt ttc gat gcg gca cgc gaa gaa ttg 480
Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
145 150 155 160

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

RECEIVED

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
245' 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

Phe Ala Glu
465

<210> 70
<211> 696
<212> DNA
<213> Neisseria gonorrhoeae

<220>
<221> CDS
<222> (1)..(693)

<400> 70
atg aaa caa tcc gcc cga ata aaa aat atg gat cag aca tta aaa aat 48
Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
1 5 10 15

aca ttg ggc att tgc gcg ctt tta gcc ttt tgt ttt ggc gcg gcc atc 96
Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
20 25 30

gca tca ggt tat cac ttg gaa tat gaa tac ggc tac cgt tat tct gcc 144
 Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
 35 40 45
 gtg ggc gct ttg gct tgc gtt gta ttt tta tta tta ttg gca cgc gcc 192
 Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
 50 55 60
 ttc cgc cgc gtt tct tca gtt gtt tta ctg att tac gtc gcc aca acc 240
 Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
 65 70 75 80
 gcc cta tat ttg cgc gtc gcc tgg ctg tat ggt gcg cct tct tat cag 288
 Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
 85 90 95
 ata gtc ggt tgc ata ttg gaa agc aat cct gcc gag cgc cgt gaa ttt 336
 Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
 100 105 110
 gtc gcc aat ctt ccc ggg tgc ctt tat ttt gtg cag gca tta ttt ttc 384
 Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
 115 120 125
 att ttt ggc ttg aca gtt tgg aaa tat tgt gta tct gtg ggg gta ttt 432
 Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe
 130 135 140
 gct gac gta aaa aac tat aaa cgt cgc agc aaa ata tgg ctg acc ata 480
 Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
 145 150 155 160
 tta ttg act ttg att ttg tcc tgc gcg gtg atg gag aaa atc gcc gcc 528
 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly
 165 170 175
 gat aaa gat tgg cga gaa cct gat gcc gcc ctg ttg ttg aat att ttc 576
 Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
 180 185 190
 gac ctg tat tac gac ttg gct ttc cgc gcc gcc aca ata tgc cgc caa 624
 Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln
 195 200 205
 gcg cgc cca cat ttt gga agc agc aaa aaa agc gtc aac atg gca tat 672
 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
 210 215 220
 ccg cca act tgc gcc caa gta taa 696
 Pro Pro Thr Cys Ala Gln Val
 225 230

<210> 71
 <211> 231
 <212> PRT
 <213> Neisseria gonorrhoeae

<400> 71
 Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
 1 5 10 15

Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
 20 25 30

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala

45

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<210> 72
<211> 2607
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(2604)

<400> 72
atg gct gcc aac caa cgt tac cgc aaa ccg ctg ccc ggt acg gat ttg 48
Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu
      1              5              10              15

gaa tac tac gac gcg cgt gcg gcg tgt gag ggc atc aaa ccc ggc tct 96
Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser
      20              25              30

tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144
Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
      35              40              45

aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
      50              55              60

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[illegible]

cag Gln 65	ctg Leu	att Ile	gag Glu	gga Gly	aaa Gly 70	cag Gln	gaa Glu	atc Ile	gac Asp	ttt Phe 75	cct Pro	tgg Trp	tat Tyr	ccg Pro	gcg Gly 80	240
cgg Arg	gtg Val	gtg Val	tgc Cys	cac His 85	gat Asp	att Ile	ctg Leu	ggg Gly	cag Gln 90	acc Thr	gcg Ala	ttg Leu	gtg Val	gat Asp 95	ttg Leu	288
gca Ala	ggt Gly	ctg Leu	cgc Pro 100	gat Asp	gcg Ala	att Ile	gcc Ala	gaa Gln 105	aaa Lys	ggc Gly	ggc Gly	gat Asp	cct Pro 110	gcc Ala	aaa Lys	336
gtg Val	aat Asn	ccg Pro 115	gtg Val	gtg Val	caa Gln	acc Thr	cag Gln 120	ctc Leu	atc Ile	gtc Val	gac Asp 125	cac His	tcg Ser	ctg Leu	gcg Ala	384
gtg Val	gaa Gln 130	tgc Cys	ggc Gly	ggc Gly	tac Tyr 135	gac Pro	ccc Pro	gat Asp	gcg Ala	ttc Phe 140	cgc Ala	aaa Lys	aac Asn	cgc Arg	gaa Glu	432
atc Ile 145	gaa Glu	gac Asp	aga Arg	cgt Arg	aac Asn 150	gaa Glu	gac Asp	cgt Arg	ttc Phe 155	cac His	ttc Phe	atc Ile	aac Asn	tgg Trp	aca Thr 160	480
aaa Lys	acc Thr	gct Ala	ttt Phe 165	gaa Glu	aat Asn	gtg Val	gac Asp	gtg Val	att Ile 170	ccg Pro	gcg Ala	ggc Gly	aac Asn	ggc Gly 175	atc Ile	528
atg Met	cac His	caa Gln 180	atc Ile	aat Asn	cta Leu	gaa Glu	aaa Lys	atg Met	tcg Ser	ccc Pro	gtc Val	gtc Val	caa Gln 190	gtc Val	aaa Lys	576
aac Asn	ggc Gly	gtg Val 195	gct Ala	ttc Phe	ccc Pro	gat Asp	acc Thr 200	tgc Cys	gtc Val	ggc Gly	acg Thr	gat Asp 205	tcg Ser	cac His	acg Thr	624
cca Pro	cac His 210	gtc Val	gat Asp	gcg Ala	ctg Leu	ggc Gly 215	gtg Val	att Ile	tcc Ser	gtg Val	ggc Gly 220	gtg Val	ggc Gly	gga Gly	ttg Leu	672
gaa Glu 225	gcg Ala	gaa Glu	acc Thr	gta Val	atg Met 230	ctg Leu	gga Gly	cgc Arg	gcg Ala	tcc Ser 235	atg Met	atg Met	cgc Arg	ctg Leu	ccc Pro 240	720
gat Asp	att Ile	gtc Val	ggc Gly 245	gtt Val	gag Glu	ctg Leu	aac Asn	ggc Gly 250	aaa Lys	cgg Arg	aag Lys	gcg Ala	ggc Gly 255	att Ile	acg Thr	768
gcg Ala	acg Thr	gat Asp	att Ile 260	gtg Val	ttg Leu	gca Ala	ctg Leu	acc Thr 265	gag Glu	ttt Phe	ctg Phe	cgc Leu	aaa Lys 270	gaa Glu	cgc Arg	816
gtg Val	gtc Val	ggg Val 275	gcg Ala	ttt Phe	gtc Val	gaa Glu	ttc Phe 280	ttc Phe	ggc Gly	gag Glu	ggc Gly	gag Ala	aga Arg	agc Ser	ctg Leu	864
tct Ser	atc Ile	ggc Gly	gac Asp	cgc Arg	gcg Ala 295	acc Thr	att Ile	tcc Ser	aac Asn	atg Met 300	acg Met	cgc Pro	gag Glu	ttc Phe	ggc Gly	912
gcg Ala	act Thr	gcc Ala	ggc Ala	atg Met 310	ttc Phe	gct Ala	att Ile	gat Asp	gag Glu	caa Gln 315	acc Thr	att Ile	gat Asp	tat Tyr	ttg Leu 320	960
aaa Lys	ctg Leu	acc Thr	cgc Gly	gac Arg	gac Asp	gac Asp	cag Ala	gtg Gln	aaa Val	ttg Lys	gtg Leu	gaa Val	acc Glu	acc Thr	tac Tyr	1008

ggg aac gcg gct tag'
Gly Asn Ala Ala
865

<210> 73
<211> 868
<212> PRT
<213> Neisseria meningitidis

<400> 73
Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu
1 5 10 15

Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser
20 25 30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
35 40 45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
50 55 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
65 70 75 80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
85 90 95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
100 105 110

Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala
115 120 125

Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu
130 135 140

Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr
145 150 155 160

Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile
165 170 175

Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys
180 185 190

Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr
195 200 205

Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu
210 215 220

Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro
225 230 235 240

Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr
245 250 255

Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Gly Arg
260 265 270

Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu
275 280 285

Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly
 290 295 300
 Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu
 305 310 315 320
 Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr
 325 330 335
 Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr
 340 345 350
 Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala
 355 360 365
 Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly
 370 375 380
 Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro
 385 390 395 400
 Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser
 405 410 415
 Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn
 420 425 430
 Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro
 435 440 445
 Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro
 450 455 460
 Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr
 465 470 475 480
 Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile
 485 490 495
 Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn
 500 505 510
 Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser
 515 520 525
 Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp
 530 535 540
 Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu
 545 550 555 560
 Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu
 565 570 575
 Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp
 580 585 590
 Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro
 595 600 605
 Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala
 610 615 620
 Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp
 625 630 635 640

aaa ttg cac cac gcg atg atg ggt acc gcc tct gtt gcc att gcg acc 960
 Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
 305 310 315 320
 gcc gcc gcc gtg ccc ggt acg ctg gtc aac ctt gcc gca gcc ggc gga 1008
 Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly
 325 330 335
 acg cgt aaa gaa gtg cgc ttc ggg cat cct tcc gcc aca ttg cgc gtc 1056
 Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
 340 345 350
 ggt gca gcc gcc gaa tgt cag gac gga caa tgg acg gcc acc aaa gcg 1104
 Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
 355 360 365
 gtt atg agc cgc agc gca cgc gtg atg atg gaa ggt tgg gtc agg gtg 1152
 Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
 370 375 380
 ccg gaa gat tgt ttt taa 1170
 Pro Glu Asp Cys Phe
 385

<210> 75

<211> 389

<212> PRT

<213> Neisseria meningitidis

<400> 75

Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser
 1 5 10 15

Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
 20 25 30

Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
 35 40 45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
 50 55 60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp
 65 70 75 80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
 85 90 95

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
 100 105 110

Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile
 115 120 125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
 130 135 140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
 145 150 155 160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
 165 170 175

<210> 80
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 80
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 <223> Description of Artificial Sequence: primer

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 <210> 83
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 <220>
 <223> Description of Artificial Sequence: primer

 <400> 83
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 <210> 84
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 <220>
 <223> Description of Artificial Sequence: primer

 <400> 84
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 <210> 85
 <211> 30
 <212> DNA
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 <220>

<223> Description of Artificial Sequence: primer

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cgggatccag aaccggtagc ctacgccgac

30

<210> 86

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 86
gctctagacc accatgaaca cacgcatcat cgtttc

36

<210> 87

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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30

<210> 88

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 88
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34

<210> 89

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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27

<210> 90

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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CG830427.001501

<210> 91
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<223> Description of Artificial Sequence: primer

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<210> 93
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<223> Description of Artificial Sequence: primer

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<210> 94
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<223> Description of Artificial Sequence: primer

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<210> 96
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<210> 97

<211> 62

<212> DNA

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<220>

<223> Description of Artificial Sequence: primer

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<210> 98

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<223> Description of Artificial Sequence: primer

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<210> 99

<211> 54

<212> DNA

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<211> 33

<212> DNA

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<223> Description of Artificial Sequence: primer

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<212> DNA

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<210> 103
<211> 30
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<220>
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<210> 105
<211> 30
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 105
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<210> 106
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<220>
<223> Description of Artificial Sequence: primer

<400> 106
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<210> 107
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<220>
<223> Description of Artificial Sequence: primer

<400> 107
cgggatccat tccgcaaata cctgtttcca acc

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<210> 108
<211> 30
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<210> 109
<211> 28
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<220>
<223> Description of Artificial Sequence: primer

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<210> 110
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 110
gctctagacc accatgaatg tttaagggtt ccc

33

<210> 111
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<212> DNA
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<220>
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<210> 112
<211> 34
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<223> Description of Artificial Sequence: primer

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<210> 113
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 <210> 114
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 <220>
 <223> Description of Artificial Sequence: primer

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 <210> 115
 <211> 32
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 <210> 116
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 <223> Description of Artificial Sequence: primer

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 <223> Description of Artificial Sequence: primer

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 <210> 118
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

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<212> DNA
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<220>
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33

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<210> 126
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<210> 127
<211> 29
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<223> Description of Artificial Sequence: primer

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29

<210> 128
<211> 36
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<210> 129
<211> 28
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<220>
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(54) Titre: ACIDES NUCLEIQUES ET POLYPEPTIDES SPECIFIQUES DES SOUCHES PATHOGENES DU GENRE NEISSERIA		
(57) Abstract		
The invention concerns nucleic acids coding for polypeptides specific of the <i>Neisseria</i> genus pathogenic strains, the corresponding polypeptides, and their diagnostic and therapeutic applications.		
(57) Abrégé		
Cette invention concerne des acides nucléiques codant pour les polypeptides spécifiques des souches pathogènes du genre <i>Neisseria</i> , les polypeptides correspondants, et leurs applications diagnostiques et thérapeutiques.		

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Nucleic acids and polypeptides specific for pathogenic strains of the *Neisseria* genus.

The present invention relates to nucleic acids encoding polypeptides specific for pathogenic strains of the *Neisseria* genus, in particular which are useful for preventing or treating a *Neisseria meningitidis* infection.

In general, meningitis is either of viral origin or of bacterial origin. The bacteria mainly responsible are: type b *Haemophilus influenzae*, *Neisseria meningitidis* and *Streptococcus pneumoniae*. The *Neisseria meningitidis* species is subdivided into serogroups according to the nature of the capsular polysaccharides. Although about a dozen serogroups exist, 90% of meningitis cases can be attributed to three serogroups: A, B and C.

Effective vaccines based on capsular polysaccharides exist for preventing meningitis caused by *Neisseria meningitidis* serogroups A and C. These polysaccharides, unmodified, are only slightly immunogenic, or not at all, in children under the age of two, and do not induce any immune memory. However, these drawbacks can be overcome by conjugating these polysaccharides to a carrier protein.

On the other hand, the polysaccharide of *Neisseria meningitidis* serogroup B is non-immunogenic, or relatively non-immunogenic in humans, whether or not it is in a conjugated form. Thus, it appears to be highly desirable to seek a vaccine against meningitis caused by *Neisseria meningitidis*, in particular *Neisseria meningitidis* serogroup B, other than a vaccine based on polysaccharide.

To this end, various proteins of the external membrane of *N. meningitidis* have already been proposed, such as the membrane-bound receptor for human transferrin (WO 90/12591 and WO 93/06861).

Neisseria meningitidis is genetically very close to *Neisseria gonorrhoeae* and *Neisseria lactamica*.

N. gonorrhoeae is especially responsible for infections located in the urogenital tract. It colonizes the genital mucous membrane, crosses the epithelium and then invades the sub-epithelium, where it multiplies and is responsible for a severe inflammatory reaction. On the other hand, *N. lactamica* is considered to be a nonpathogenic species.

Sequences present in *N. gonorrhoeae* and *N. meningitidis*, but absent from *N. lactamica*, have been disclosed in patent application WO 98/02547, but this prior patent application does not locate or identify the coding sequences.

The authors of the present invention have now managed to identify some of these genes by searching, in the meningococcal genome, for the open reading frames specific for pathogenic strains of the *Neisseria* genus, using the following strategy:

Some of the sequences disclosed in patent application WO 98/02547 (referred to, in said prior application, as SEQ ID Nos 66, 67, 69, 70, 72 to 96, 98 and 99) were positioned on the sequence of the genome of the *N. meningitidis* serogroup B strain (ATCC 13090), available from the Pathoseq® bank of Incyte Pharmaceuticals, and also on the sequence of the genome of the *Neisseria meningitidis* strain Z2491 (Sanger Centre). This made it possible to identify, in the *N. meningitidis* genome which has 2.3 mega bases, 19 contigs representing 220 000 base pairs.

The authors of the present invention then analysed, for each of the 19 contigs, the presence of open reading frames (ORFs) containing at least 100 amino acids (and, by definition, bordered by an initiation codon and a stop codon), using the Gene Jockey II sequence processor® program (Biosoft). This analysis made it possible to select approximately 400 candidate ORFs.

The sequences of each of these ORFs were then analysed using the Codon Use® program (Conrad Halling), which takes into account the codon use frequency in

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N. meningitidis. Only the ORFs with sequences having a maximum frequency of use of these codons were selected. At the end of this analysis, 197 candidate ORFs were selected.

5 The ORFs selected using this double analysis
were subjected to a homology search through all of the
available banks, using the BLASTX® program, from the
access to the Pathoseq® bank of Incyte Pharmaceuticals.
This homology search made it possible to exclude the
10 ORFs encoding, *a priori*, cytoplasmic or periplasmic
proteins, in particular metabolism proteins. The ORFs
were also subjected to analysis of possible protein
motifs, using the DNA Star Protean® program (Lasergene
software).

15 The authors of the present invention then investigated whether the ORFs selected at the end of the previous step (118 in number) were effectively absent from *N. lactamica*, as predicted by the application of the prior art WO 98/02547.

20 To this end, a PCR amplification was carried out. This amplification proved to be ineffective for 78 of the 118 ORFs tested. Only the ORFs for which the amplification in *N. lactamica* was negative (sequences named "lactamica-") were selected. In order to verify
25 that these negative results were not "false negatives", the lactamica- sequences selected were subjected to a control by dot blot. At the end of this step, only 23 ORFs were confirmed *N. meningitidis**/*N. lactamica*.

Finally, these 23 ORFs were repositioned in their entirety on the *N. meningitidis* ATCC13090 genome. This made it possible to demonstrate that three ORFs previously eliminated on the basis of their putative protein function appeared to be located close to, or were even framed by, some of the 23 *N. meningitidis*⁺/*N. lactamica*⁻ ORFs. These three ORFs (SEQ ID Nos 29, 35 and 37) were reintroduced into the study, and it was proven that they were also *N. meningitidis*⁺/*N. lactamica*⁻.

The authors of the present invention then attempted to discover whether the ORFs identified using the genome of the *N. meningitidis* serogroup B strain ATCC 13090 were also present in the genomes of
5 *N. meningitidis* serogroup A Z2491 (Sanger Centre) and of *N. gonorrhoeae* FA1090 (Advanced Centre of Genome Technology, Oklahoma University). Then, they compared the sequences derived from these various genomes, with multiple alignment (Clustal, Infobiogen). This made it
10 possible to redefine, for some of the ORFs, the most probable position of the initiation codon and translation stop codon. The sequences of the open reading frames derived from the strain ATCC13090 are given in the SEQ ID Nos 1-51 (odd numbers) and the
15 amino acid sequences which are deduced therefrom are given in the SEQ ID Nos 2-52 (even numbers).

A subject of the present invention is, therefore, a nucleic acid in isolated form encoding a polypeptide, or an antigenic fragment thereof,
20 excluding the nucleic acids disclosed in SEQ ID Nos 70, 73, 74, 77, 80, 81, 87, 88, 89, 94, 95 and 98 of application WO 98/02547 (sequences attached to the present description and numbered SEQ ID Nos 70A, 73A, 74A, 77A, 80A, 81A, 87A, 88A, 89A, 94A, 95A and 98A so
25 as to distinguish them from the sequences of the invention); said polypeptide having an amino acid sequence which is identical or homologous to a sequence selected from those of group II; group II consisting of the sequences shown in SEQ ID Nos 2-52 (even numbers)
30 and the sequence SEQ ID No. 53.

Preferably, said nucleic acid can have a nucleotide sequence selected from those of group I, group I consisting of the sequences shown in SEQ ID Nos 1-51 (odd numbers).

35 The term "nucleic acid" includes and means equally ORF, gene, polynucleotide, DNA and RNA. The term "nucleic acid in isolated form" means a nucleic acid separated from the biological environment in which it is found under natural conditions. For example, a

modifications (for example phosphorylation or glycosylation).

The expression "antigenic fragments of the polypeptides specific for pathogenic strains of the *Neisseria* genus" is intended to mean the polypeptides derived from the polypeptides of the invention as defined above, through deletions of portions of said polypeptides without destroying the antigenicity (for example, without notable loss of the antigenic activity) of said polypeptides. The specific antigenicity can be determined using various methods known to those skilled in the art, as explained later.

These fragments are preferably at least 12 amino acids long, more preferably at least 20 amino acids long, preferentially 50 amino acids long, more preferably still 75 amino acids long, preferentially 100 amino acids long.

These fragments can be used to reveal epitopes which may be masked in the parent polypeptides. They are also advantageous for inducing a T-lymphocyte-dependent protective immune response. The deletions can, in fact, make it possible to eliminate immunodominant regions which are highly variable between various strains.

Such fragments can be obtained using standard techniques known to those skilled in the art (for example, Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons Inc, 1994), for example by PCR, RT-PCR or treatment with restriction enzymes for the cloned DNA molecules, or by the method of Kunkel et al. (Proc. Natl. Acad. Sci. USA (1985) 82:448).

The expression "homologous amino acid sequence" is intended to mean a sequence which differs from one of the sequences of group II by substitution, deletion and/or insertion of one or more amino acids, at positions such that these modifications do not destroy the specific antigenicity of the polypeptide in question.

Advantageously, a homologous amino acid sequence has at least a 75% degree of homology (i.e. of identity) with one of the sequences of group II; preferably this degree of homology is at least 80%, most preferably at least 90%. The homologous amino acid sequences include, in particular, the sequences which are substantially identical to one of the sequences of group II. The expression "substantially identical sequence" means a sequence which has at least a 90%, advantageously at least a 95%, preferably at least a 97%, and most preferably at least a 99%, degree of homology (i.e. of identity) with one of the sequences of group II. In addition, it may differ from the reference sequence only through mainly conservative substitutions.

The degree of homology (also named degree of identity) is generally determined using a sequence analysis program (for example, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Centre, 1710 University Avenue, Madison, WI 53705). Similar amino acid sequences are aligned so as to obtain the maximum degree of homology (i.e. identity). To this end, it may be necessary to artificially introduce gaps into the sequence. Once optimal alignment has been produced, the degree of homology (i.e. identity) is established by recording all the positions for which the amino acids

of the two sequences compared are identical, with respect to the total number of positions.

The expression "homologous nucleotide sequences" is intended to mean sequences which differ from the sequences of group I by substitution of one or more nucleotides, or by deletion and/or insertion of one or more codons, at positions such that these sequences (i) still encode polypeptides having the sequences of group II, due to the effect of the degeneracy of the genetic code; or (ii) encode polypeptides having homologous sequences as defined above.

Advantageously, a homologous nucleotide sequence has at least a 60% degree of homology with one
15 of the sequences of group I; preferably this degree of homology is at least 80%, most preferably at least 90%.

Typically, a homologous nucleotide sequence hybridizes specifically to the sequences complementary to the sequences of group I, under stringent conditions. The temperature at which the hybridization assay is carried out constitutes an important factor which influences the stringency. Conventionally, this temperature, termed hybridization temperature (T_h), is selected from 5 to 40°C, preferably from 20 to 25°C, below the temperature at which 50% of the paired strands separate (T_m). In general, it is considered that conditions of high stringency are satisfied when T_h is lower than T_m by 5 to 25°C approximately, for example by 5 to 10°C or, most commonly, by 20 to 25°C approximately. Moderate stringency is established when T_h is lower than T_m by 30 to 40°C.

For sequences comprising more than 30 bases, the temperature T_m is defined by the equation: $T_m = 81.5 + 0.41(\%G+C) + 16.6 \log(\text{cation concentration}) - 0.63(\% \text{formamide}) - (600/\text{number of bases})$. Thus, ionic strength has a major impact on the value of T_m . The temperature T_m increases by 16.6°C every time the monovalent cation concentration increases by a factor of 10. The addition of formamide into the hybridization

buffer causes, on the other hand, the value of T_m to decrease. (For a complete reference, see Sambrook et al., Molecular Cloning, A laboratory manual, Cold Spring Harbor Laboratory Press, 1989, pages 9.54-9.62).

5 Conventionally, hybridization experiments are carried out at a temperature of 60 to 68°C, for example at 65°C. At this temperature, stringent hybridization conditions can, for example, be implemented in 6xSSC, advantageously in 2xSSC or 1xSSC, preferably in
10 0.5xSSC, 0.3xSSC or 0.1xSSC (in the absence of formamide). A solution of 1xSSC contains 0.15 M of NaCl and 0.015 M of sodium citrate.

For this reason, in other words, a subject of the invention is a polynucleotide in isolated form,
15 which is capable of hybridizing, under stringent conditions, with a DNA molecule having one of the nucleotide sequences as shown in SEQ ID Nos 1-51 (odd numbers) or the sequences complementary thereto.

A specific class of homologous sequences
20 consists of those encountered naturally by virtue of the extremely common phenomenon of allelic variation. A bacterial species, for example *N. meningitidis* or *N. gonorrhoeae*, consists of a large variety of strains which differ from one another through minor variations,
25 termed allelic variations. Thus, a polypeptide which is present in various strains and which, of course, performs the same biological function in each of them, can have an amino acid sequence which is not identical from one strain to the other. In other words, the
30 sequences derived from the allelic variation are purely sequences equivalent or alternative to those of group II. The class of sequences which are allelic variants of one of the sequences of group II consists of the sequences of the polypeptide as found in a
35 pathogenic species of the *Neisseria* genus (for example, *N. meningitidis* or *N. gonorrhoeae*) other than the *N. meningitidis* strain ATCC 13090. The biological function which is associated with the allelic variant sequences is the same as that which is associated with

the reference sequence. The differences (substitution, deletion or addition of one or more amino acids) which they exhibit between one another (including the reference sequence) do not modify the biological function of the polypeptide. The term "biological function" is intended to mean the function exercised by the polypeptide in the cells which produce it naturally.

The allelic variation is also expressed in the coding sequences. A polynucleotide, encoding a polypeptide, having a sequence which is an allelic variant of one of the sequences of group I can be easily cloned by amplifying the genomic DNA of the strains of pathogenic species of the *Neisseria* genus, for example by PCR (polymerase chain reaction), using synthetic oligonucleotide primers capable of hybridizing to the 5' and 3' ends of the coding region. The sequences of such primers can easily be established by those skilled in the art using the nucleotide sequences given in SEQ ID Nos 1-51 (odd numbers). The primers generally have from 10 to 40 nucleotides, preferably from 15 to 25 nucleotides.

For this reason, in other words, a subject of the invention is a DNA molecule in isolated form which can be amplified and/or cloned by PCR from the genome of a pathogenic *Neisseria* strain, using a pair of 5' and 3' PCR primers; the sequences of these primers being established using one of the nucleotide sequences as shown in SEQ ID Nos 1-51 (odd numbers). An example is given, for each pair of primers, in Example I.1 hereinafter.

A subject of the present invention is more particularly the allelic variants having the nucleotide sequences SEQ ID Nos 54 to 76 (even numbers) and the products encoded by these nucleotide sequences, having the amino acid sequences SEQ ID Nos 55 to 77 (odd numbers).

The polypeptides of the invention can be fused to other polypeptides, for example by translation of a

hybrid gene. Vectors for expressing fusion polypeptides are commercially available, such as the vectors pMal-c2 or pMal-p2 from New England Biolabs, in which the protein to which the polypeptides of the invention can be fused is a maltose-binding protein, the glutathione-S-transferase system from Pharmacia or the His-Tag system from Novagen. Such systems are in particular useful for purifying the polypeptides of the invention. The polypeptides of the invention can be fused to polypeptides having adjuvant activity, such as for example the B subunit of cholera toxin or the B subunit of the *E. coli* heat-sensitive toxin.

The nucleic acids of the present invention can be used (i) in a process for producing the polypeptides encoded by said nucleic acids, in a recombinant host system, (ii) for the construction of vaccination vectors, such as poxviruses, intended to be used in methods and compositions for preventing and/or for treating an infection with pathogenic *Neisseria* strains, in particular with *Neisseria meningitidis*, (iii) as a vaccination agent in a naked form or in combination with a vehicle which promotes transfer to the target cells and, (iv) in the construction of attenuated *Neisseria* strains which can overexpress a nucleic acid of the invention, or express it in a non-toxic, mutated form.

The present invention also provides (i) an expression cassette containing a polynucleotide of the invention placed under the control of elements allowing its expression, in particular under the control of a suitable promoter; (ii) an expression vector containing said expression cassette; (iii) a host cell (prokaryotic or eukaryotic) transformed with an expression cassette and/or an expression vector as defined above, and (iv) a method for obtaining a polypeptide encoded by said polynucleotide of the invention, comprising culturing said transformed cell under conditions allowing the expression of the

polynucleotide of the invention, and recovering the polypeptide from the cell culture.

Among the eukaryotic hosts which can be used, mention may be made in particular of yeast cells (for example *Saccharomyces cerevisiae* or *Pichia Pastoris*), mammalian cells (for example COS1, NIH3T3 or JEG3) arthropod cells (for example *Spodoptera frugiperda* (SF9)) and plant cells. Among the prokaryotic hosts which can be used, mention may be made in particular of *E. coli*.

The choice of the expression cassette depends on the host system chosen, and also on the characteristics desired for the expressed polypeptide. In general, expression cassettes include a promoter which is functional in the host system selected and which can be constitutive or inducible; a ribosome-binding site; an initiation codon (ATG); if necessary, a region encoding a signal peptide; a nucleotide sequence of the invention; a stop codon; and, optionally, a 3' terminal region (translation and/or transcription terminator). The open reading frame (ORF) consisting of the nucleotide sequence of the invention, alone or associated with the region encoding the signal peptide, is placed under the control of the promoter such that translation and transcription take place in the host system. The promoters and regions encoding the signal peptides are known to those skilled in the art. Among them, mention may be made in particular of the arabinose-inducible promoter (araB promoter) of *Salmonella typhimurium*, which is functional in Gram⁻ bacteria such as *E. coli* (US 5,028,530 and Cagnon et al., Protein Engineering (1991) 4(7): 843), the promoter of the T7 bacteriophage gene encoding RNA polymerase (US 4,952,496), and the *OspA* and *RlpB* signal peptide (Takase et al., J. Bact. (1987) 169:5692).

The polypeptide expressed can be recovered in a practically purified form from the cell extract or from the supernatant, after centrifuging the recombinant cell culture. The recombinant polypeptide can, in

particular, be purified using methods of affinity purification with the aid of antibodies, or using any other method known to those skilled in the art, for instance by genetic fusion with a small binding domain.

5 The nucleic acids of the invention can also be used in the field of vaccination, either by using a viral or bacterial host as a vehicle for releasing the DNA, or by administering the nucleic acid of interest in a free form.

10 A subject of the present invention is also (i) a vaccination vector containing a nucleic acid of the invention, placed under the control of elements allowing its expression; (ii) a pharmaceutical composition containing a therapeutically or
15 prophylactically effective amount of said vaccination vector; (iii) a method for inducing an immune response against *Neisseria* in a vertebrate, in particular a mammal, preferably a human, said method comprising the administration to said vertebrate of an immunologically
20 effective amount of said vaccination vector so as to cause an immune response, in particular a protective or therapeutic response to *Neisseria meningitidis*; and (iv) a method for preventing and/or treating an infection with pathogenic *Neisseria* strains, in
25 particular with *Neisseria meningitidis*, which comprises the administration of a prophylactic or therapeutic amount of said vaccination vector of the invention to an individual requiring such a treatment.

30 In combination with the polypeptides of the invention, the vaccination vector as defined above can also comprise nucleotide sequences the expression of which allows the immune response to be stimulated, such as the sequences encoding cytokines.

35 Said vaccination vector of the invention can be administered via any route which is conventional in the field of vaccination, in particular via the parenteral route (for example subcutaneous, intradermal, intramuscular, intravenous or intraperitoneal route). The dose depends on many parameters which are known to

those skilled in the art, such as the vector itself, the route of administration, or the weight, age or sex of the animal or of the human to be vaccinated.

A subject of the present invention is also (i) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a polynucleotide of the invention; (ii) a method for inducing an immune response against pathogenic *Neisseria* strains, in particular *Neisseria meningitidis* in a vertebrate, by administering to said vertebrate an immunologically effective amount of said polynucleotide so as to cause an immune response, in particular a protective immune response against pathogenic *Neisseria* strains, especially *Neisseria meningitidis*; and (iii) a method for preventing and for treating an infection with pathogenic *Neisseria* strains, in particular with *Neisseria meningitidis*, by administering a therapeutic or prophylactic amount of said polynucleotide to an individual requiring such a treatment.

The polynucleotides of the invention (DNA or RNA) can be administered to a vertebrate as they are. When a DNA molecule of the invention is used, it can be in the form of a plasmid incapable of replicating in a vertebrate cell and incapable of integrating the genome of said vertebrate. Said DNA molecule is, typically, placed under the control of a promoter suitable for expression in a vertebrate cell. Said polynucleotide used as vaccine can be formulated according to various methods known to those skilled in the art. Said polynucleotide can, in particular, be used in a naked form, free of any vehicle which promotes transfer to the target cell, such as anionic liposomes, cationic lipids, microparticles, for example gold microparticles, precipitation agents, for example calcium phosphate, or any other agent which facilitates transfection. In this case, the polynucleotide can be simply diluted in a physiologically acceptable solution, such as a sterile solution or a sterile

buffer solution, in the presence or absence of a vehicle. When it is present, this vehicle can be preferably isotonic, hypotonic or slightly hypertonic, and has a relatively low ionic strength. It can, for example, be a sucrose solution (for example a solution containing 20% of sucrose).

Alternatively, a polynucleotide of the invention can be combined with agents which facilitate transfection. It can be, inter alia, (i) combined with a chemical agent which modifies cell permeability, such as bupivacain (WO 94/16737); (ii) encapsulated in liposomes, optionally in the presence of additional substances which facilitate transfection (WO 93/18759, WO 93/19768, WO 94/25608 and WO 95/2397, WO 93/18759 and WO 93/19768); or (iii) combined with cationic lipids, or silica, gold or tungsten microparticles.

When the polynucleotides of the invention coat microparticles, these particles can be injected via the intradermal or intraepidermal route, using the "gene gun" technique (US 4,945,050, US No. 5,015,580 and WO 94/24263).

The amount of DNA to be used as a vaccine depends, in particular, on the strength of the promoter used in the DNA construct, on the immunogenicity of the product expressed, on the individual to which this DNA is administered, on the method of administration and on the type of formulation. In general, a therapeutically or prophylactically effective amount ranging from approximately 1 µg to approximately 1 mg, preferably from approximately 10 µg to approximately 800 µg, and preferentially from approximately 25 µg to approximately 250 µg, can be administered to human adults.

The polynucleotide of the invention can be administered via any conventional route of administration, such as in particular via the parenteral route. The choice of the route of administration depends, in particular, on the formulation chosen. A polynucleotide formulated in

combination with bupivacain is advantageously administered into muscle. When neutral or anionic liposomes, or a cationic lipid such as DOTMA (N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethylammonium chloride) or DC-Chol (3-beta-(N-(N',N'-dimethylaminomethane)carbamoyl)cholesterol) are used, the formulation can advantageously be injected via the intravenous, intramuscular, intradermal or subcutaneous route. A polynucleotide in a naked form can advantageously be administered via the intramuscular, intradermal or subcutaneous route.

The nucleotide sequences of the invention allow the construction of specific nucleotide probes and primers which can be used in diagnosis. Said probes or primers are nucleic acids having sequences identical or homologous to portions of the sequences of group I or to the sequences complementary thereto.

Preferably, said probes contain from approximately 5 to approximately 100, preferably from approximately 10 to approximately 80, nucleotides. They can contain modified bases, the sugar and phosphate residues possibly also being modified or substituted. The probes of the invention can be used in diagnostic tests, to capture or detect polynucleotides specific for pathogenic *Neisseria* strains. Such capture probes can conventionally be immobilized on a solid support directly or indirectly, by covalent bonding or by passive adsorption. A detection probe can be labelled, in particular with a radioactive isotope, an enzyme such as peroxidase or alkaline phosphatase, or enzymes capable of hydrolyzing a chromogenic, fluorogenic or luminescent substrate, or with compounds which are, themselves, chromogenic, fluorogenic or luminescent, nucleotide analogues; or biotin.

A primer generally contains from approximately 10 to approximately 40 nucleotides, and can be used to initiate enzymatic polymerization of the DNA in an amplification process (for example PCR), in an elongation process or in a reverse transcription

method. A primer of the invention can in particular be a primer as described in Example II.1 hereinafter.

A subject of the present invention is also:

- (i) a reagent containing a probe of the invention for detecting and/or identifying the presence of pathogenic *Neisseria* strains in a biological sample;
- (ii) a process for detecting and/or for identifying the presence of pathogenic *Neisseria* strains in a biological sample, said method comprising the steps consisting in a) extracting the DNA or RNA from a biological sample and denaturing it; b) exposing said DNA or said RNA to a probe of the invention, under stringent hybridization conditions, so as to detect the hybridization; and
- (iii) a method for detecting and/or for identifying pathogenic *Neisseria* strains in a biological sample, in which the DNA is extracted from a biological sample and mixed together with at least one and preferably with two primers of the invention, and is amplified, for example by PCR.

As mentioned above, the polypeptides produced by the expression of the ORF sequences identified can be used as vaccination agents. The specific antigenicity of the polypeptides homologous to the polypeptides having sequences of group II can be evaluated by assaying the cross-reactivity with an antiserum directed against the polypeptides having sequences of group II. A monospecific hyperimmune antiserum can be produced against a purified polypeptide having a sequence of group II or a fusion polypeptide, for example an expression product of the MBP, GST or His-tag systems.

The specific antigenicity can be determined using various methods known to those skilled in the art, in particular the Western blot, dot blot and ELISA techniques, described below.

In the Western blot technique, the protein preparation to be tested is subjected to SDS-PAGE gel electrophoresis. After transfer onto a nitrocellulose

membrane, the material is incubated with a monospecific hyperimmune antiserum obtained after having immunized an animal with the referent material; i.e., in the present case, with a polypeptide having an amino acid sequence of group II. This antiserum is diluted
5 beforehand in a dilution range of approximately 1:50 to 1:5000, preferably of approximately 1:100 to 1:500. The specific antigenicity is revealed when a band corresponding to the product shows reactivity with one
10 of the dilutions above.

In the ELISA assay, a purified protein preparation is preferably used, although a whole cell extract may also be used. Approximately 100 μ l of a preparation at approximately 10 μ g/ml are distributed
15 into the wells of a plate. The plate is incubated for two hours at 37°C, and then overnight at 4°C. The plate is then washed with a phosphate buffered saline solution (PBS) comprising 0.05% of Tween 20. The wells are saturated with 250 μ l of PBS containing 1% of
20 bovine serum albumin (BSA) so as to prevent non-specific antibody binding. After incubation for one hour at 37°C, the plate is washed with the PBS/Tween buffer. The antiserum is serially diluted in PBS/Tween buffer containing 0.5% BSA. 100 μ l of this dilution are
25 added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, when specific antibodies are produced in rabbits, a goat anti-rabbit peroxidase conjugate is added to the wells. The incubation is
30 carried out for 90 minutes at 37°C and the plate is then washed. The reaction is measured by colorimetry (the reaction is positive when the optical density value is 1, if the dilution is at least 1:50, preferably at least 1:500).

In the dot blot assay, a purified protein is
35 preferably used, it being understood that it is also possible to use a whole cell extract. Two-fold serial dilutions of a protein solution at approximately 100 μ g/ml are prepared in a 50 mM Tris-HCl buffer,

20

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The immunogenic compositions of the invention can be administered via any route which is conventional in the field of vaccination, in particular via the parenteral route (for example subcutaneous,

intradermal, intramuscular, intravenous or intraperitoneal route). The choice of the route of administration depends on a certain number of parameters, such as the adjuvant combined with the polypeptide.

A composition of the invention contains at least one polypeptide as defined above. It can also contain at least one additional antigen of *Neisseria meningitidis* and/or *Neisseria gonorrhoeae*.

The polypeptides of the invention can be formulated with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS or "virus-like" particles, in order to facilitate the transfer of the polypeptide and/or to increase the immune response.

The administration can be carried out with a single dose or with doses repeated, if necessary, at intervals which can be determined by those skilled in the art.

For example, an initial dose can be followed by three booster doses at intervals of one or more weeks or of one or more months. The suitable dose depends on many parameters, including the individual treated (adult or child), the specific vaccination antigen, the route of administration and the frequency of administration, the presence or absence or the type of adjuvant, and the desired effect (for example protection and/or treatment), and can be determined by those skilled in the art. If the route of administration is parenteral, the dose is preferentially less than 1 mg, preferably approximately 100 µg. The polypeptides and polynucleotides of the invention used as vaccination agents can be used sequentially, in a several-step immunization process. For example, a vertebrate can be initially sensitized with a vaccination vector of the invention, such as a poxvirus, for example via the parenteral route, and can then be stimulated twice with the polypeptide encoded by the vaccination vector.

A polypeptide of the invention can also be useful as a diagnostic agent for detecting the presence of anti-*Neisseria meningitidis* and/or anti-*Neisseria gonorrhoeae* antibodies in a biological sample such as a blood sample.

A subject of the present invention is also monospecific antibodies directed against the polypeptides of the invention.

The term "monospecific antibodies" is intended to mean an antibody capable of reacting specifically with a *Neisseria* polypeptide of the invention. Such antibodies can be polyclonal or monoclonal, and can be recombinant antibodies, for example chimeric (for example consisting of a variable region of murine origin associated with a constant region of human origin), humanized and/or single-chain antibodies. Said antibodies can also be in the form of immunoglobulin fragments, for example F(ab)'2 or Fab fragments. The antibodies of the invention can be of any isotype, for example IgA or IgG, the polyclonal antibodies possibly being of a single isotype or possibly containing a mixture of several isotypes.

The antibodies of the invention directed against the polypeptides of the invention can be produced and identified using standard immunological methods, for example Western blot analysis, a dot blot assay, an ELISA assay (Coligan et al., Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). Said antibodies can be used in diagnostic processes for detecting the presence of a *Neisseria meningitidis* antigen in a sample such as, in particular, a biological sample (for example a blood sample).

The antibodies of the invention can also be used in affinity chromatography processes for purifying a polypeptide of the invention. Finally, such antibodies can also be used in prophylactic or therapeutic passive immunization methods.

A subject of the present invention is also a diagnostic method for detecting the presence of pathogenic *Neisseria* strains in a biological sample, comprising bringing said biological sample into contact
5 with an antibody or a polypeptide of the invention, such that an immune complex is formed, and detecting said complex which indicates pathogenic *Neisseria* strains in the organism from which the sample originates. Those skilled in the art understand that
10 the immune complex is formed between a component of the sample and the antibody or the polypeptide of the invention, any substance not bound possibly being eliminated prior to the detection of the complex.

Thus, a reagent of polypeptide type can be used
15 for detecting the presence of anti-*Neisseria meningitidis* and/or *Neisseria gonorrhoeae* antibodies in a sample, whereas an antibody of the invention can be used as a reagent for assaying the presence of a *Neisseria meningitidis* and/or *Neisseria gonorrhoeae*
20 polypeptide in a sample.

For use in diagnostic applications, the reagent (for example the antibody or the polypeptide of the invention) can be in the free state or immobilized on a solid support, by direct or indirect means.

25 The direct means include passive adsorption or covalent bonding between the support and the reagent.

The term "indirect means" is intended to mean that a substance which interacts with said reagent is attached to the solid support. For example, if a
30 reagent of polypeptide type is used, an antibody which binds to this polypeptide can be used as an anti-reagent substance, it being understood that this substance binds to an antibody which is not involved in recognizing the antibodies in the biological samples.

35 Among the indirect means which can be used, mention may also be made of the ligand receptor system, a molecule such as a vitamin possibly being grafted onto the reagent of polypeptide type, and the corresponding receptor possibly being immobilized on

the solid phase. This is illustrated by the biotin-streptavidin system. It is also possible to add a peptide tail to the reagent, by chemical engineering or genetic engineering, and to immobilize the grafted or fused product by passive adsorption or covalent bonding with the peptide tail.

A subject of the present invention is also a process for purifying, from a biological sample, a *Neisseria* polypeptide of the invention, by affinity chromatography with a monospecific antibody of the invention. Said antibody is preferably of isotype IgG.

According to an example of implementation, a biological sample, preferably in a buffer solution, is applied to a chromatographic material, preferably equilibrated with the buffer used to dilute the biological sample, such that the polypeptide of the invention (i.e. the antigen) may adsorb to the material. The unbound components are washed and the antigen is then eluted with a suitable elution buffer, such as a glycine buffer or a buffer containing chaotropic agent, for example guanidine HCl, or a high concentration of salt (for example 3 M MgCl₂). The eluted fractions are recovered and the presence of antigen is detected, for example by measuring the absorbance at 280 nm.

A subject of the present invention is also (i) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a monospecific antibody of the invention; and (ii) a method for preventing and/or for treating an infection with pathogenic *Neisseria* strains, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an individual requiring such a treatment.

To this end, the monospecific antibody of the invention is preferably of isotype IgG, and preferably fixes the complement. Said monospecific antibody according to the invention can be administered alone or in a mixture with at least one other monospecific

antibody, specific for a different *Neisseria meningitidis* and/or *Neisseria gonorrhoeae* polypeptide, according to the invention. The amount of antibody can be determined easily by those skilled in the art. For
5 example, a daily administration of approximately 100 to 1000 mg of antibodies over a week, or three daily doses of approximately 100 to 1000 mg of antibodies over two or three days, may be an effective dose.

The therapeutic or prophylactic effectiveness
10 may be evaluated using standard methods known to those skilled in the art, for example by measuring the induction of an immune response or the induction of protective and/or therapeutic immunity (in newborn rats or mice), through evaluation of the bacterial load in
15 the cerebrospinal fluid. The protection can be determined by comparing the degree of *Neisseria* infection to a control group. Protection is demonstrated when the infection is decreased in comparison with the control group. Such an evaluation
20 can be carried out with the polynucleotides, the vaccination vectors, the polypeptides and also the antibodies according to the invention. The therapeutic or prophylactic effectiveness of a product according to the invention (polynucleotide or polypeptide) can also
25 be evaluated in an assay for bactericidal activity, as described by Danve et al., Vaccine (1993) 11(12):1214 against the meningococcal strain of origin of the polynucleotide or polypeptide used. In the field of meningococcal vaccines, the bactericidal activity assay
30 is, in fact, recognized as being the reference assay based upon which it is possible to make a valid prediction of the vaccination value of a product. Briefly, a product according to the invention is administered to animals such as rabbits in order to
35 produce an antiserum against this product. Then, this antiserum is assayed for its lysis capacity. The bactericidal titre of an antiserum represents the inverse of the dilution of this antiserum for which 50% of the load of meningococci is lysed. The antiserum is

considered to be bactericidal when the titre is higher than 4, with respect to the meningococcal strain of origin of the polynucleotide or polypeptide used. In that case, the product against which the antiserum was generated is demonstrated to be potentially advantageous from a pharmaceutical point of view.

The following examples illustrate the invention without limiting the scope thereof.

10 Legend of the figure

The attached figure represents the vector pCAMyc-His used as a cloning vector.

15 Details of the strategy for identifying the

ORFs:

In order to select the ORF sequences specific for the pathogenic strains of the *Neisseria* genus, a PCR amplification is carried out on the sequences of the 118 ORFs selected after analysis with the Gene Jockey®, Codon Use®, and homology search programs. Only the sequences for which the amplification in *N. lactamica* is negative (sequences named "lactamica") are selected. In order to verify that these negative results are not "false negatives", the lactamica sequences selected are subjected to a dot blot.

A - PCR amplification:

A.1. Extraction of genomic DNAs:

The genomic DNAs of all of the *Neisseria* strains used in this study were prepared according to an identical protocol. The *N. meningitidis*, *N. lactamica*, *N. flava*, *N. subflava* and *N. mucosa* strains were cultured on tissues of MHA (Muller Hinton Agar, Difco) medium, and the *N. gonorrhoeae* were cultured on tissues of MHA medium supplemented with 10% of heat-treated horse blood (Biomérieux) and 1% of Isovitalex (Biomérieux). The culturing is carried out under an atmosphere containing 10%

CO₂, overnight at 37°C. Then, the cells are harvested, and washed in PBS phosphate buffer (pH 7.2), and the DNA is extracted according to protocol D of the "Rapid Prep genomic DNA isolation kit for cells and tissue" (Pharmacia Biotech).

The genomic DNAs were then controlled on agarose gel for their completeness and by PCR reaction for their purity.

A.2. PCR reaction for screening the ORFs absent in *N. lactamica* 2314:

A PCR amplification was carried out on the genomic DNAs of the *N. meningitidis* strain ATCC 13090 and *N. lactamica* strain 2314 (ATCC 23970), according to the following protocol:

The PCR reaction was carried out on a 50 µl volume with 10 ng of genomic DNA, 250 µM of each of the dNTPs, 300 nM of each of the primers, 1X Taq DNA polymerase buffer and 2 u of Taq DNA polymerase (Appligène).

The amplification cycles are:

	97°C	45 seconds	25 cycles
25	56°C	1 minute	25 cycles
	72°C	2.30 minutes	25 cycles

For each of the ORFs analysed, positive and negative controls for the PCR reaction were carried out. At this stage, only the *N. meningitidis*+ and *N. lactamica*- ORFs are selected.

B - Selection of the *N. meningitidis** *N. lactamica* ORFs by dot blot on genomic DNA:

The absence of a product of PCR amplification of an ORF with genomic DNA of *N. lactamica* 2314 as the matrix does not guarantee the absence of this ORF in the *N. lactamica* 2314 genome. Specifically, a certain variability in the region to which the oligonucleotides

In this context, further verification is carried out by dot blot on genomic DNA, using, as probe, the products of genomic amplification on the *N. meningitidis* strain corresponding to each of the reading frames identified. The dot blot filters contain genomic DNA of the following strains: 2 *N. lactamica* strains 8064 and 2314, one *N. flava* strain ATCC 30008,

The dot blot technique used is as follows.
20 Approximately 50 ng of genomic DNA, denatured for 5 min
at 100°C, of the various *Neisseria* strains are loaded,
with suction, onto a Hybond N+ nitrocellulose membrane
(Amersham) placed between the jaws of a dot blot
apparatus (BioRad). Then, the DNA is fixed on the
25 membranes for 5 min with UV radiation at 315 nm.

The ORF which does not hybridize to the genomic DNA of *N. lactamica* 2314 and 8064 is definitively
35 selected as a potential vaccination candidate.

Example I: Cloning

1. PCR amplification

5 Each of the ORFs was amplified by PCR using the genomic DNA of *N. meningitidis* serogroup B (strain ATCC 13090), according to standard protocol.

Two oligonucleotides, primers on the N-terminal side and on the C-terminal side were defined for each
10 of the ORF sequences of the invention.

The primer on the N-terminal side comprises an enzyme restriction site for cloning, a CCACC Kozak sequence for translation initiation (M. Kozak, J. Mol. Biol. 196: 947-950), the ATG of the potential ORF and
15 approximately 17 bases specific for the 5' portion of the ORF.

The primer on the C-terminal side was defined such that the ORF cloned is in fusion, in its 3' portion, with a repeat of 8 histidines and a stop codon
20 which are present in the vector behind the multiple cloning site, hence the insertion of an "A" base in order to keep the correct reading frame after cloning and the disappearance of the stop codon of the ORF. The primer on the C-terminal side thus comprises an enzyme
25 restriction site for cloning, an "A" base, and then approximately 20 bases specific for the 3' portion of the gene starting from the codon preceding the stop codon.

After searching for restriction sites which are
30 absent in each of the ORFs, with the aid of the DNASTAR MapDraw subprogram (Lasergene Software), the XbaI restriction site in 5' and BglII restriction site in 3' are used for the ORF SEQ ID No. 19. For the ORF SEQ ID No. 41, the SpeI site in 5' and the BglII site in 3'
35 are used. The XbaI restriction site in 5' and BamHI restriction site in 3' are used to clone the remaining ORFs.

The PCR mixture comprises, for a final volume of 100 µl, 10-50 ng of genomic DNA, the N-terminal and

C-terminal primers each at 200 nM, the dNTPs each at 250 μ M, the 1X PCR buffer (composition of the 10X PCR buffer: 200 mM Tris-HCl (pH 8.8), 20 mM MgSO_4 , 100 mM KCl, 100 mM $(\text{NH}_4)_2\text{SO}_4$, 1% TritonX-100 and 1 mg/ml of 5 nuclease-free bovine serum albumin) and 2.5 U of polymerase.

The amplification is carried out as follows:

Step	Temperature (°C)	Time (min.)	Number of cycles
Denaturation	97	0.45	25
Hybridization	cf. table	1	25
Elongation	72	1/kb DNA	25

ORF No. (internal ref.)	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization T ₀
22	1-2 N.g allelic variant: 54, 55	GCTCTA GAC CAC CAT GTC TGA AGA AAA ATT GAA AAT GAG (SEQ ID n° 78)	CGG GAT CCA GAA ATG GCT GGA TTC GCT ATC AG (SEQ ID n° 79)	Tfu (Appligene)	56°C
41	3-4	GCTCTA GAC CAC CAT GAA ACA CTT ACT CAT CG (SEQ ID n° 80)	CGG GAT CCA ATA CTT AGG ACT TGG GTC (SEQ ID n° 81)	Tfu (Appligene)	43°C
42-43	5-6 N.g allelic variant: 56, 57	GCTCTA GAC CAC CAT GAA AAA ATC CCT TTT CGT TC (SEQ ID n° 82)	CGG GAT CCA TTG CCG ATA AAC ATA TTC CAC C (SEQ ID n° 83)	Tfu (Appligene)	56°C
47	7-8 N.g allelic variant: 58, 59	GCTCTA GAC CAC CAT GCG AAC GAC CCC AAC CTT C (SEQ ID n° 84)	CGG GAT CCA GAA CCG GTA GCT TAC GCC GAC (SEQ ID n° 85)	Tfu (Appligene)	56°C
55	9-10 N.g allelic variant: 60, 61	GCTCTA GAC CAC CAT GAA CAC ACG CAT CAT CGT TTC (SEQ ID n° 86)	CGG GAT CCA GCA ACG GGC TGT CAC TTT AAG (SEQ ID n° 87)	Pfu Turbo (Stratagene)	56°C
68	11-12	GCTCTA GAC CAC CAT GCT GAC GTT TAT CGG ACT G (SEQ ID n° 88)	CGG GAT CCA CCG CAG AGG CAC GAT TCC (SEQ ID n° 89)	Tfu (Appligene)	56°C

ORF No. (internal ref.)	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization T°
71	13-14	GCT CTA GAC CAC CAT GGG CAT CTA TCT GGA GTT C (SEQ ID n° 90)	CGG GAT TCA CAA AAG TTC CAG AAA AIC TAA CTC (SEQ ID n° 91)	Tfu (Appligene)	56°C
72	15-16 N.mA. allelic variant: 62, 63	GCT CTA GAC CAC CAT GAA TAG ATC CAA GCA ACC (SEQ ID n° 92)	CTG GAT CCA TGC CCG TTG GGG GAG GC (SEQ ID n° 93)	Pfu Turbo (Stratagene)	56°C
73	17-18 N.g allelic variant: 64, 65	GCT CTA GAC CAC CAT GAT GAA TGT GTA GGC AGA G (SEQ ID n° 94)	CGG GAT TCA CAG TTT GCC CGA CAT AC (SEQ ID n° 95)	Pfu Turbo (Stratagene)	56°C
74	19-20	GCT CTA GAC CAC CAT GAA ATT TTT TTC TGC TCA (SEQ ID n° 96)	GAA GAT CTA GAA ACT GTA ATT CAA GTT GAA G (SEQ ID n° 97)	Pfu Turbo (Stratagene)	56°C
98	21-22	GCT CTA GAC CAC CAT GAT TGA ATT TGT CCG AGC (SEQ ID n° 98)	CGG GAT CCA ACC CAG CUA CTA GTT (SEQ ID n° 99)	Pfu Turbo (Stratagene)	56°C
116	23-24 N.g.allelic variant: 66, 67	GCT CTA GAC CAC CAT GCA ATA CAG CAC ACT GAC (SEQ ID n° 100)	CGG GAT CCA CTC CTT TTT CCG ACC TTG AAG (SEQ ID n° 101)	Pfu Turbo (Stratagene)	56°C
122	25-26	GCT CTA GAC CAC CAT GCA CCA GTC GGG CAA ATT C (SEQ ID n° 102)	CGG GAT CCA AGC TGT TTG GCG ATT TGG GTG (SEQ ID n° 103)	Pfu Turbo (Stratagene)	56°C

ORF No. (internal ref.)	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization T°
125	27-28	GCT CTA GAC CAC CAT GAA AAA GGG CGG GCG AAA GC (SEQ ID n° 104)	CGG GAT CCA GTG CCT GCG CAG CTT GGA ATC (SEQ ID n° 105)	Pfu Turbo (Stratagene)	56°C
128	29-30 N.mA. allelic variant: 68, 69	GCT CTA GAC CAC CAT GAC ATT GGT CAA TGT AAT GAT AAT G (SEQ ID n° 106)	CGG GAT CCA TTC CGC AAA TAC CTG TTT CCA ACC (SEQ ID n° 107)	Tfu (Appligene)	56°C
152	31-32 N.g allelic variant:	GCT CTA GAC CAC CAT GAA AYA ATC CGC CTG (SEQ ID n° 108)	CGG GAT CCA TAC TTG GGC GCA ACA TAA C (SEQ ID n° 109)	Pfu Turbo (Stratagene)	56°C
153	70, 71 33-34	GCT CTA GAC CAC CAT GAA TGT TTA CGG TTT CTT (SEQ ID n° 110)	CGG GAT CCA TTT TTT AGA CGT AAT TTT AGT CG (SEQ ID n° 111)	Tfu (Appligene)	56°C
155	35-36	GCT CTA GAC CAC CAT GAT GAG TCA ACA CTC TGC C (SEQ ID n° 112)	CGG GAT CCA TCC AGT TTT TGC TCG AAG GC (SEQ ID n° 113)	Tfu (Appligene)	56°C
156	37-38	GCT CTA GAC CAC CAT GGC TTC GAG CAA AAA CTG G (SEQ ID n° 114)	CGG GAT CCA TCG TTC TTT AAT CTC CAC AAA CG (SEQ ID n° 115)	Tfu (Appligene)	56°C
157	39-40	GCT CTA GAC CAC CAT GCA CC TGG AAA G (SEQ ID n° 116)	CGG GAT CCA TTC AAT TCG CTT CAA CAA TG (SEQ ID n° 117)	Tfu (Appligene)	56°C

ORF No. (internal ref.)	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization T°
158	41-42 N.mA. allelic variant: 72, 73	GGG CTA GTC CAC CAT TGG TGT CAA CCA AGC TTA TCG (SEQ ID n° 118)	GAA GAT CTA AGC CGC GHT CUC TTC CAA AAA ATC (SEQ ID n° 119)	Tfu (Appligene)	56°C
159	43-44 N.mA. allelic variant: 74, 75	GGT GTA GAC CAC CAT TCC GCA AAT TAA AAT TTT C (SEQ ID n° 120)	CGG GAT CCA AAA ACA ATC TTC CGG CAC CC (SEQ ID n° 121)	Tfu (Appligene)	56°C
161	45-46	GGT CTA GAT CAC GAT GGG CAC GAT GTT TTG TTG (SEQ ID n° 122)	CGG GAT CCA TTG GGC AAC GAC GAA GGC AC (SEQ ID n° 123)	Tfu (Appligene)	56°C
163-1	47-48	GGT CTA GAC CAC CAT GAG AAT AGA GAT CAC ACC (SEQ ID n° 124)	CGG GAT CCA TGG CTC AAT CCT TTC TGC (SEQ ID n° 125)	Pfu Turbo (Stratagene)	56°C
163-2	49-50	GGT CTA GAC CAC CAT GAT TAA GGT TTC GGC AGT G (SEQ ID n° 126)	CGG GAT CCA ACC TGC TTC ATG GGT CAT TTC (SEQ ID n° 127)	Tfu (Appligene)	56°C
167-168	51-52 N.gallelic variant: 76, 77	GGT CTA GAC CAC CAT GAA TTC GAC CGC AAG TAA AAC (SEQ ID n° 128)	CGG GAT CCA AAT CCC TCT GCC GTA TTT G (SEQ ID n° 129)	Tfu (Appligene)	56°C

2- Cloning, transformation and selection of recombinants

The cloning vector used is the 6.357 kb vector pCA/Myc-His or pM1070 (cf. figure), derived from the plasmid pCDNA 3.1 (Invitrogen). pCA/Myc-His comprises, in particular, the CMV iel promoter (bases 249-902), intron A of the CMV iel gene (Chapman et al., 1991 Nucleic Acids Research, 19, 3979-3986), a multiple cloning site (bases 1792-1852) with the PmlI, EcoRV, NotI, XbaI, BamHI, KpnI and HindIII sites, a sequence encoding a polyhistidine and a stop codon (bases 1908-1928), a bgh 3' termination sequence (bases 1853-2197) and the ampicillin resistance gene for selecting the recombinant clones in *E. coli*.

After purification (GeneClean Bio101 kit), the PCR amplification products are digested for 2 hours at 37°C with the appropriate enzymes (XbaI-BamHI, XbaI-BglII or SpeI-BglII), in a final reaction volume of 20 µl. The digestion products are then ligated with the vector pCA/Myc-His, digested beforehand with XbaI and BamHI, according to the "Rapid DNA Ligation Kit" protocol (Boehringer Mannheim). 15 µl of the ligation is used to transform 100 µl of competent *E. coli* XLI-blue cells (Novagen). The cells are incubated for 30 minutes in ice, 30 seconds at 42°C and 2 minutes in ice. Then, 500 µl of LB medium without antibiotics are added, and the mixture is incubated for 1 hour at 37°C. Next, 50 and 550 µl of the culture are plated out on plates containing LB medium plus ampicillin (50 µg/ml final concentration), and incubated overnight at 37°C.

The following day, 36 colonies are placed in culture in 2 ml of LB plus ampicillin (50 µg/ml) and incubated overnight at 37°C.

The following day, the plasmid DNA is extracted according to the Qiagen mini-prep protocol (Qiagen) and the recombinants are identified by enzymatic restriction followed by agarose gel electrophoresis. The cloning junctions are then verified by sequencing.

Example II: Evaluation of the protective activity of the ORFs of the invention

5 A. Preparation of the DNA intended for the immunization experiments:

An isolated colony of a recombinant clone is used to inoculate a preculture in LB medium + ampicillin, and 5 ml of this preculture represents the
10 inoculum of a 2.5 litre culture in LB medium + ampicillin. The purification protocol for preparing the plasmid DNA is that described in the EndoFree Giga Kit (Qiagen). The purified DNA is eluted from the
15 purification column with a 10 mM Tris-HCl, 1 mM EDTA buffer, pH 8, and stored at -20°C. Before injection, the purified recombinant plasmid is diluted to 100 µg/ml with water (of injectable preparation quality) and the NaCl concentration is brought to 150 mM.

20

B. Production of a specific polyclonal serum:

B.1. Hyperimmunization in an animal model:

25 The animal model used is the mouse or the rabbit. The route of administration of the injected DNA is the intramuscular or intradermal route. The recombinant plasmids to be injected are optionally applied to beads if they are injected into animals
30 using a gene gun apparatus (BioRad). The immunization protocol follows a scheme comprising two injections, 3 weeks apart.

35 B.2. Analysis of the bactericidal activity of the antibodies induced:

Ten days after the final injection, the animals are bled and the sera are analysed using the bactericidal activity assay according to the protocol of Danve et al., Vaccine (1993) 11 (12):1214. Briefly,

the sera are incubated at various dilutions (2-fold) in the presence of rabbit complement and of meningococci cultured in the presence or absence of an iron-chelating agent. The bactericidal titre of a serum represents the inverse of the dilution of this antiserum for which 50% of the bacteria are lysed.

It is considered that the antiserum is not bactericidal when its titre is lower than 4 against the homologous strain.

When the bactericidal titre corresponds to a 4-fold seroconversion against the homologous strain, the bactericidal activity of the antiserum is analysed against other *Neisseria* strains in order to measure the extent of the cross-reactivity of the antiserum of interest.

Example III: Production of purified recombinant proteins

1. Recombinant production of proteins

a. Preparation of transformants:

The PCR product obtained is then digested at 37°C for two hours with restriction enzymes, in 20 µl of reaction volume. The digestion product is ligated into a plasmid pET28a (Novagen) which is cleaved in a similar way and which is dephosphorylated, before ligation, by treating with calf intestine alkaline phosphatase. The fusion gene constructed in this way allows the one-step affinity purification of the resulting fusion protein, due to the presence of histidine residues at the N-terminal end of the fusion protein, which are encoded by this vector.

The ligation reaction (20 µl) is carried out at 14°C overnight, before transforming 100 µl of fresh competent *E. coli* XL1-blue cells (Novagen). The cells are incubated on ice for two hours, and then subjected to a heat shock at 42°C for 30 seconds, before being returned to the ice for 90 seconds. The samples are

then added to 1 ml of LB broth without selection, and cultured at 37°C for two hours. The cells are then plated out on LB agar medium supplemented with kanamycin (50 µg/ml final concentration) at a 10^x dilution, and are incubated overnight at 37°C. The following day, 50 colonies are subcultured on secondary plates and are incubated at 37°C overnight.

b. Production of the protein:

The stored transformants (10 µl) are plated out onto selection plates and cultured overnight at 37°C. A few cells are harvested from the plate and used as an inoculum for an overnight starter culture (3 ml) at 37°C. The following day, a sample (time T = 0) is taken and centrifuged at 14 000 rpm for 3 minutes. The starter culture is then used to inoculate an LB medium containing kanamycin (100 µg/ml) at a dilution of 1:50 (starting optical density OD₆₀₀ = 0.05-0.1). The cells are cultured to an OD₆₀₀ of 1.0, a sample is taken for SDS-PAGE (pre-induction sample) and the remaining culture is induced with 1 mM of IPTG. The cultures are cultured for four hours and samples are taken every hour. The culture is centrifuged at 600 g for 20 minutes at 4°C. The supernatant is discarded and the pellets are resuspended in 50 mM of Tris-HCl (pH: 8.0), 2 mM EDTA, and recentrifuged. The supernatant is discarded and the cells are stored at -70°C.

2. Protein purification

The pellets obtained from one litre of culture prepared according to Example I.4 above are dried and resuspended in 20 ml of 20 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 5 mM imidazole, cooled in ice. Lysozyme is added at a concentration of 0.1 mg/ml, and the suspension is homogenized using a high-speed homogenizer (Turrax), then treated with a sonicator (Sonifier 450, Branson). Benzonase (Merck) is used at a final concentration of 1 U/ml in order to eliminate the DNA. The suspension is centrifuged at 40 000 g for 20 minutes and the

supernatant is filtered through a 0.45 μ m membrane. The supernatant is loaded onto an IMAC column (12 ml of resin) which has been prepared by immobilizing Ni⁺⁺ cations according to the manufacturer's recommendations (Pharmacia). The column is washed with 10 column volumes of 20 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 60 mM imidazole. The recombinant protein is eluted with six volumes of 20 mM Tris-HCl (pH: 7.9), 0.5 M NaCl, 500 mM imidazole, 0.1% Zwittergent 3-14.

The elution profile is controlled by measuring the absorbance of the fractions at an optical density of 280 nm. An aliquot fraction is analysed on an SDS-PAGE gel and stained with Coomassie blue (Phast System - Pharmacia), and the fractions corresponding to the protein peak are then pooled and concentrated. In order to eliminate the elution buffer, the fraction is passed over a G24 Sephadex column (Pharmacia) and equilibrated in PBS buffer (pH: 7.4). The protein solution is sterilized by filtration through a 0.45 μ m membrane, and the protein concentration is determined using the BCA micromethod (Pierce). The protein solution is stored at -70°C.

Example IV: Production of monospecific

polyclonal antibodies

1. Rabbit hyperimmune antiserum

100 μ g (in total) of the polypeptide purified in Example III, in the presence of complete Freund's adjuvant in a total volume of approximately 2 ml, are injected into New Zealand rabbits, both subcutaneously and intravenously. 21 and 42 days after the initial injection, the booster doses, which are identical to the initial doses, are administered in the same way, with the exception that incomplete Freund's adjuvant is used. 15 days after the final injection, the animal's serum is recovered, decomplexed and filtered through a 0.45 μ m membrane.

2. Mouse hyperimmune ascites fluid

10-50 µg of the purified fusion polypeptide obtained in Example II, in the presence of complete Freund's adjuvant, in a volume of approximately 200 µl, are injected subcutaneously into 10 mice. 7 and 14 days after the initial injection, booster doses, which are identical to the initial doses, are administered in the same way, with the exception that incomplete Freund's adjuvant is used. 21 and 28 days after the initial injection, the mice receive 50 µg of the antigen alone, intraperitoneally. On the 21st day, the mice are also injected intraperitoneally with 180/TG CM26684 sarcoma cells (Lennette & Schmidt, Diagnostic procedures for viral, rickettsial, and chlamydial infections, (1979) 5th Ed. Washington DC, American Public Health Association). The ascites fluids are harvested 10 to 13 days after the first injection.

20 Example V: Purification of the polypeptides of the invention by immunoaffinity

1. Purification of specific IgG

An immune serum as prepared in Example IV is applied to a Fast Flow Sepharose 4 protein A column (Pharmacia) equilibrated with 100 mM Tris-HCl (pH: 8.0). The resin is washed by applying 10 column volumes of 100 mM Tris-HCl and 10 volumes of 10 mM Tris-HCl (pH: 8.0) to the column. The IgGs are eluted with a 0.1 M glycine buffer (pH: 3.0) and are collected by 5 ml fraction, to which 0.25 ml of 1 M Tris-HCl (pH: 8.0) are added. The optical density of the eluate is measured at 280 nm and the fractions containing the IgGs are pooled and, if necessary, stored at -70°C.

35 2. Column preparation

A suitable amount of CNBr-activated Sepharose 4B gel (1 g of dried gel providing approximately 3.5 ml of hydrated gel, and the capacity of the gel ranging from 5 to 10 mg of coupled IgG per ml of gel)

manufactured by Pharmacia (17-0430-01) is suspended in 1 mM HCl buffer and washed, using a Buchner funnel, by adding small amounts of 1 mM HCl buffer. The total volume of the buffer is 200 ml per gram of gel.

- 5 The purified IgGs are dialysed for four hours at $20 \pm 5^\circ\text{C}$ against 5 volumes of 500 mM PBS buffer (pH: 7.5). Then, they are diluted in 500 mM of PBS (pH: 7.5) for a final concentration of 3 mg/ml.

- 10 The IgGs are incubated with the gel overnight at $5 \pm 3^\circ\text{C}$, with stirring. The gel is packed into a chromatography column and washed with 2 column volumes of 500 mM phosphate buffer (pH: 7.5) and then one volume of 50 mM NaCl sodium buffer (pH: 7.5). The gel is then transferred to a tube, then incubated with
15 100 mM of ethanolamine (pH: 7.5) for 4 hours at room temperature with stirring, and then washed twice with two column volumes of PBS. The gel is then stored in PBS merthiolate at 1/10 000. The amount of IgG coupled to the gel is determined by measuring the optical
20 density at 280 nm of the IgG solution and of the direct eluate.

3. Adsorption and elution of the antigen

- 25 A solution of antigen in 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA, for example the supernatant obtained in Example III.2 after treatment with Benzonase, centrifugation and filtration through a 0.45 μm membrane, is applied to a column equilibrated with 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA, at a flow
30 rate of approximately 10 ml/hour. Then, the column is washed with 20 volumes of 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA. Alternatively, batch adsorption can be carried out, in which the mixture is left overnight at $5 \pm 3^\circ\text{C}$, with stirring.

- 35 The gel is washed with 2 to 6 volumes of 10 mM PBS buffer (pH: 6.8). The antigen is eluted with a 100 mM glycine buffer (pH: 2.5). The eluate is collected in 3 ml fractions, to which 150 μl of 1 mM PBS buffer (pH: 8.0) are added. The optical density is

measured at 280 nm for each fraction; those containing the antigen are recovered and stored at -20°C.

09630437.051601

Fragments of the genome of *N. meningitidis* Z2491
described in patent application WO 98/02547

(2) INFORMATION FOR SEQ ID NO: 70A:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70A:

GATCAGACCC ATTTTCAGCG CACCGTAAGC GCGGATTTTC TCGAATTTT CCAAAGCTGC	60
GGCATCGTGT TTGATGTGCT CTGCAACTC TTTCGCCGTG TAGCCCAAGT CGCGGGCATT	120
CAGGAAAACG GTCGGAATG CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG	180
CACATCAATT TCATCGACCA AATTGCCGCT TGGGAACATA CTGCTTCGC CGTCGGCTGG	240
ATC	243

20

(2) INFORMATION FOR SEQ ID NO: 73A:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

30

(iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73A:

5

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60
ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 74A:

10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO

20

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74A:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60
ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

25

(2) INFORMATION FOR SEQ ID NO: 77A

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

35

09530433.001601

(iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77A:

CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG	60
ATTTTATTTC GAGATCGGT CGGAACAGAA GGAAGAAAA ACAAGCCTCC CCGTGGGAA	120
GAATCCAAAC GGGTAAAAAA GGCCTTGGTA AATTGGCATT ATTGGGGCTT GGCAACAAAA	180
TTGAAATTTC TACTATCCAG GGAACGAAA GGGTTACTTT TACTTTGGAT TATGCAGAGA	240
TTGGAAGAAG CAAGGGTATT TATCAACCG	269

(2) INFORMATION FOR SEQ ID NO: 80A:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80A:

CGGGTCGCTT TATTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG TTTGGAANTA	60
TTGTGTATCG GGGGGGGGTA TTGCTGACG TAAAAAATA TAAACGCCGC GCAAAATATG	120
GCTGACTATA TTATTGACTT TGATTTTGTG CTGCGCGGTG ATGGATAAAA TCGCCAGCGA	180
TAAAGAATTT GCGAGAACCT GATGCCG	207

25

(2) INFORMATION FOR SEQ ID NO: 81A:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81A:

CGGCAACGAT TTGAGCTATC GCGGTTACGA CATTCTGGAT TTGGCACAAA AATGCGASTT	60
TGAAGAAGTC GCCCACTCTC TGATTCAAGG CCATCTGCCC AACAAATTCG AGCTGGCCGC	120
TTATAAACC AAGCTCAAA CCATGCGCGG CTGCTCTC CTTCTGATTA AAGTTTGGGA	180
AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCCT ACGG	224

(2) INFORMATION FOR SEQ ID NO: 87A:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

30 (iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87A:

09530433.DAT

AATTTCACC	TATGCCCTAC	GCAGCGATTA	TCCGTGGTTT	ACCCAAAGGG	TGATTATGGC	60
AAAAGCCCGG	GTTTGAGCGA	CCGCCCTTTG	TTGCCGGCGT	TCAAACGGGT	TTTGATAGGA	120
AATGCAGGCA	CGAAGCCTCG	GCTGATTGTG	ATGCACCTGA	TGGGTTGCGA	CAGTGATTTT	180
TGCACACGTT	TGGATAAGGA	TGGCGGCGCG	TTTCAGTATC	AAACTGAAA	AATATCCTGC	240
TATGTTTCCA	TCAATCGCGC	AAACCGATAA	ATT			273

(2) INFORMATION FOR SEQ ID NO: 88A:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88A:

AATTCCTCCG	CACGGGGAGG	CTTGTTTTC	TTCCCTTCG	TTCCGACCGA	TTCTCAAATA	60
AAAAATCATG	ATTTCATCGA	AGTTCAATCC	TATACCATTAA	TCTTTAATAA	CGATTTTATG	120
CTCCGGTTTA	TGCAATAACC	TAACCTCCAC	TTCCGTAGCA	CATGCATCGT	AGGCATTCGC	180
TATCAACTCG	GCAATCGCAO	GAACAGTGIG	CGAATACAAT	CTTTACACCC	AAATGTTTGA	240
TTACGGTTCG	CTCGAAACTC	AATTTCAATT				270

20

(2) INFORMATION FOR SEQ ID NO: 89A:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89A:

AATTATGAAC ACAGGCATCA TCGTTTCGGC TCGTTTCGTT GCGTTGGCAT TAGCAGGTTG	50
CGGCTCAATC AATAATGTAA CCGTTTCGGA CCAGAAACTT CAGGAACGTG CCGCGTTTGC	100
CTTGGGCGTC ACCAATGCCG TAAAAATCAG CAACCCGAGC AATGAAGGCA TAGCATCAA	150
CTTTACCGCA ACTGTGGGTA AGCGCGTGAC CAATGCTATG TTACCACTGT AATCAGCACA	200
ATCGGCGGTA CCACTTCGGA TGCAATT	267

(2) INFORMATION FOR SEQ ID NO: 94A:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25 (iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94A:

AATTTGTTGG GCAGATGGCC GTGAATCAGC AGGTGGGGCA CTTCCTCAAA CTGCGATTTT	60
TGTGCGAAAT CCAGATGTTC GTAACCGCGA TACGTCAAAT CGTTGCCGGT ACGCAACGGT	120
ACACAAAGCG GTATTACGG CCGCAACGCC AGAAAGCGCA ACGGATTTT AGGTTTGAGS	180
GTGCGGGTTT GAGTAGTTTC AGTCATGGTA TTTCTCCTT GTGTTTTTAT GGGTTTCGGG	240
TTTTCAGACG ACCGATGCGG ATTTGTTGAA AGGCACTCTG AAAGCGGTAA ATCATTTTTG	300
AAACAATT	308

(2) INFORMATION FOR SEQ ID NO: 95A:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTISENS: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95A:

AATTCGAGG AGCAGTACCG CCAAGCGTTG CTCGCCTATT CCGCGGTGA TAAACAGAC	60
GAGGATATCC GCCTGATGCA ACAGAGCGAT TACGSCAACT TGTCCTACCA CATCCGTAAT	120
AAAAACATGC TTTCATTTT TTCGCAAGC AATGACGCAC AAGCTCAGCC CAACACAACT	180
GACCCATTGG CCATTTTATG AAAAAGACGC TCAAAAAGGC ATTATCACAG TTGAGGCGT	240
AGACCGCAGT GSAGAAAAAT TCAATGGCTC CAACCATTCG GGAATT	286

20

(2) INFORMATION FOR SEQ ID NO: 98A:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs

(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98A:

AATTTGTCGG CAATCTTCCC GGGTCGCTTT ATTTGTGCA GGCATTATTT TTCATTTTTG	60
GCTTGACAGT TTGGAGATAT TGTGTATCGG GGGGGGGTAT TTGCTGACGT AAAAAACTAT	120
AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTG CTGCCCGGTG	180
ATGGATAAAA TCGCCAGCBA TAAAGATTG CGAGAACCTG ATGCCGGCCT GTTGTGAAT	240
ATTTTCGACC TGTAAATTACG ATTGGCTTC CGCGCGGCA CAATATGCCG CCAAGCGGCG	300
CCCACATTTT GGAAGC	316

CLAIMS

1. Nucleic acid in isolated form, encoding a polypeptide specific for the pathogenic strains of the
5 *Neisseria* genus, or antigenic fragment thereof, excluding the sequences SEQ ID Nos 70A, 73A, 74A, 77A, 80A, 81A, 87A, 88A, 89A, 94A, 95A and 98A, the amino acid sequence of said specific polypeptide being identical or homologous to a sequence selected from the
10 sequences of group II, group II consisting of the sequences SEQ ID No. 2 to SEQ ID No. 52 (even numbers) and the sequence SEQ ID No. 53.
2. Nucleic acid according to Claim 1, the nucleotide sequence of which is identical or homologous
15 to a sequence selected from the sequences of group I, group I consisting of the sequences SEQ ID No. 1 to SEQ ID No. 51 (odd numbers).
3. Nucleic acid according to Claim 1, encoding a polypeptide specific for the pathogenic strains of the
20 *Neisseria* genus, or antigenic fragment thereof, the amino acid sequence of said specific polypeptide being selected from the sequences SEQ ID Nos 55 to 77 (odd numbers).
4. Nucleic acid according to Claim 3, having a
25 nucleotide sequence selected from the sequences SEQ ID Nos 54 to 76 (even numbers).
5. Polypeptide specific for the pathogenic strains of the *Neisseria* genus, and antigenic fragments thereof, the amino acid sequence of said specific
30 polypeptide being identical or homologous to a sequence selected from the sequences of group II, consisting of the sequences SEQ ID No. 2 to SEQ ID No. 52 (even numbers) and the sequence SEQ ID No. 53.

6. Polypeptide according to Claim 5, specific for the pathogenic strains of the *Neisseria* genus, and antigenic fragments thereof, the amino acid sequence of said specific polypeptide being selected from the sequences SEQ ID Nos 55 to 77 (even numbers).

7. Expression vector comprising an expression cassette in which a nucleotide sequence as defined in one of Claims 1 to 4 is placed under conditions allowing its expression in a host cell.

8. Host cell transformed with the expression vector according to Claim 7.

9. Pharmaceutical composition comprising:

a) a nucleic acid according to one of Claims 1 to 4, in naked form or in combination with at least one agent facilitating transfection;

b) or a vaccination vector comprising a nucleotide sequence as defined in one of Claims 1 to 4, such as in particular a virus or a bacterium;

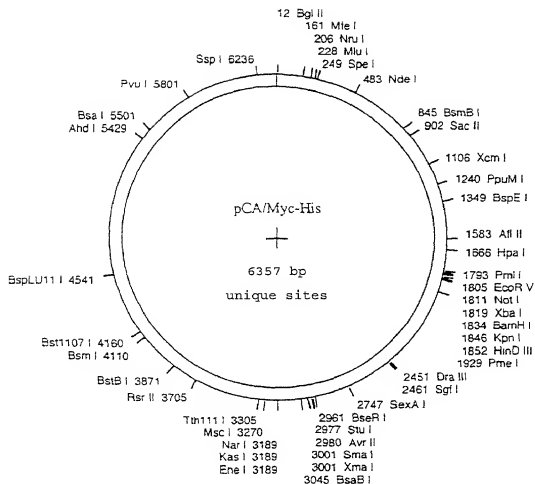
c) or a polypeptide according to either of Claims 5 and 6;

optionally in combination with a pharmaceutically acceptable vehicle.

10. Monospecific antibody directed against a polypeptide according to either of Claims 5 and 6.

11. Use of a nucleic acid according to one of Claims 1 to 4, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, according to either of Claims 5 and 6, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.

1/1



DECLARATION FOR USA PATENT APPLICATION

(including Design and National Stage PCT)

Attorney's Docket ID: _____

As a below named inventor, I hereby declare that:

My residence, mailing address and citizenship are as stated below adjacent to my name. I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought

on the invention entitled: Nucleic acids and polypeptides specific of the Neisseria genus
the specification of which: pathogenic strains

is attached hereto.

☒ was filed on

26.04.2001

as U.S. Application No. or PCT International Application No.

09/830433

and (if applicable) was amended on _____

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment specifically referred to above. I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. 119(a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT International application which designated at least one country other than the United States of America, listed below and have also identified below, where priority is not claimed, any foreign application for patent or inventor's certificate, or any PCT International application, having a filing date before that of the application on which priority is claimed. ☐ ADDITIONAL APPLICATIONS IDENTIFIED ON ATTACHED SHEET

Prior Foreign Application No.

Country

Day/Month/Year Filed

Priority Not Claimed

FR 98 13693

FRANCE

30.10.98

I hereby claim the benefit under 35 U.S.C. 120 of any U.S. application(s), or 365(c) of any PCT application designating the U.S., listed below; and insofar as the subject matter of each claim of this application is not disclosed in the prior U.S. or PCT application in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56 which became available between the filing date of the prior application and the national or PCT filing date of this application. ☐ ADDITIONAL APPLICATIONS IDENTIFIED ON ATTACHED SHEET

U.S. or PCT Parent Application No.

Parent Filing Date (Day/Month/Year)

Parent Patent No. (if applicable)

PCTFR99/02643

28.10.1999

As a named inventor, I hereby appoint the registered practitioners of LARSON & TAYLOR, PLC associated with Customer Number 000881 to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith. Direct all correspondence to that Customer Number.

Customer No 000881

Direct all telephone calls to _____ at TEL (703) 739-4900 (Fax: 703-739-9577) e-mail: _____

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. 1000 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

SOLE OR FIRST INVENTOR		Citizenship
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SIGN AND DATE HERE Inventor's Signature	<i>[Signature]</i>	Date
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		31.7.2001
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		10.07.2001
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SIGN AND DATE HERE Inventor's Signature	<i>[Signature]</i>	Date
		11.07.2001

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11/98

(7)
over

DECLARATION FOR USA PATENT APPLICATION

(including Design and National Stage PCT)

ADDITIONAL INFORMATION SHEET
(use as required)

I hereby claim the benefit under 35 U.S.C. 119(e) of any United States PROVISIONAL application(s) listed below.

U.S. Provisional Application No.

Parent Filing Date (Day/Month/Year)

Additional Prior Foreign Application(s)

Prior Foreign Application No.

Country

Day/Month/Year Filed

Priority Not Claimed

Additional 35 U.S.C. § 120 application(s)

U.S. or PCT Parent Application No.

Parent Filing Date (Day/Month/Year)

Parent Patent No. (if applicable)

Additional Joint Inventor(s):

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Inventor's Signature



Date

20 June 2001

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DATE HERE

Inventor's Signature



Date

7 June 2001

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Family Name

or Surname

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same as above

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DATE HERE

Inventor's Signature



Date

19 June 2001

EIGHTH JOINT INVENTOR
(if any)

Citizenship

Family Name

or Surname

Given Name (first

and Middle (if any))

Full Mailing

Address

Residence - City, State/Country

(if different from PO address)

SIGN AND

DATE HERE

Inventor's Signature

Date

09/830433

531 Rec'd PCT

26 APR 2001

WO 00/26375

- 1 -

PCT/FR99/02643

SEQUENCE LISTING

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INSERM

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pathogenic strains of the Neisseria genus

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 Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
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Lys Tyr Asp Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
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Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
 225 230 235 240

Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys
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Arg Arg Pro Asp Ala Phe Arg Pro Cys Arg Leu His Asn Leu Arg Gln
165 170 175

Asn Leu Arg Lys His Ile Leu Ser Asp Leu Phe Lys Glu Lys Thr Asp
180 185 190

Glu Glu Cys Glu Ile Thr Thr Ala Asn Val Ile Asn Lys Leu Lys Ala
195 200 205

Gln Asn Phe Ile Ser Ile Asp Glu Gln Glu Thr Val Ser Tyr His Leu
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Ser Asp Asn Asp Leu Leu Gln Arg Ile Gln Arg His Ile Leu Ser Gln
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Arg His Leu Arg Asp Gln Asn Leu Ile Arg Gln Asn Asn Gly Lys Ile
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Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly
65 70 75 80

Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro
85 90 95

Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr
100 105 110

Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly
 435 440 445
 Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly
 450 455 460
 Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala
 465 470 475 480
 Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile
 485 490 495
 Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu
 500 505 510
 His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser
 515 520 525
 Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys
 530 535 540
 Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser
 545 550 555 560
 Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu
 565 570 575
 Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu
 580 585 590
 Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Met Thr
 595 600 605
 Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu
 610 615 620
 Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly
 625 630 635 640
 Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu
 645 650 655
 Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr
 660 665 670
 Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala
 675 680 685
 Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly
 690 695 700
 Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser
 705 710 715 720
 Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp
 725 730 735
 Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala
 740 745 750

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<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(336)

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Met Asn Thr Arg Ile Ile Val Ser Ala Ala Phe Val Ala Leu Ala Leu
1 5 10 15

gca ggt tgc gcc tca atc aat aat gta acc gtt tcc gac cag aaa ctt 96
Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu
20 25 30

cag gaa cgt gcc gcg ttt gcc ttg gcc gtc agc caa aat gcc gta aaa 144
Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
35 40 45

atc agc aac cgc agc aat gaa agc ata cgc atc aac ttt acc gca act 192
Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr
50 55 60

gtg ggt aag cgc gtg agc caa tgc tat gtt acc agt gta atc agc aca 240
Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr
65 70 75 80

atc gcc gtt acc act tcc gat gca att tgt ttg gga gcc gga acg cac 288
Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His
85 90 95

aaa gcc aaa agt caa tgc aat gct ttg ctt aaa gcg gca gcc cgt tgc 336
Lys Gly Lys Ser Gln Cys Asn Ala Leu Leu Lys Ala Ala Gly Arg Cys
100 105 110

taa 339

<210> 10

<211> 112

<212> PRT

<213> Neisseria meningitidis

<400> 10

Met Asn Thr Arg Ile Ile Val Ser Ala Ala Phe Val Ala Leu Ala Leu
1 5 10 15

Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu
20 25 30

Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
35 40 45

Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr

145	Ser	Ser	Ala	Gly	Leu	Ile	Asn	Leu	Leu	Pro	Trp	Gly	Gly	Pro	Thr	
					150					155					160	
GGG	CGG	gtt	gca	agc	gtg	ttg	ggc	gca	gat	gtg	ggc	gaa	ttg	tat	aaa	529
Gly	Arg	Val	Ala	Ser	Val	Leu	Gly	Ala	Asp	Val	Gly	Glu	Leu	Tyr	Lys	
			165						170					175		
cct	ttg	ttg	acg	gtg	caa	att	atc	ggt	gtg	gtg	ttt	atc	ctt	gcg	ctg	
Pro	Leu	Leu	Thr	Val	Gln	Ile	Ile	Gly	Val	Val	Phe	Ile	Leu	Ala	Leu	576
			180					185					190			
tcc	ctg	ctt	ttg	ggc	gtg	cgt	gaa	aaa	agg	cgg	att	gtc	cgg	gag	ttg	624
Ser	Leu	Leu	Leu	Gly	Val	Arg	Glu	Lys	Arg	Arg	Ile	Val	Arg	Glu	Leu	
			195				200					205				
ggc	gcg	ttg	ccc	gcc	gtg	gcg	gat	ttg	ata	aag	ccg	gtg	ccc	ttg	tcg	672
Gly	Ala	Leu	Pro	Ala	Val	Ala	Asp	Leu	Ile	Lys	Pro	Val	Pro	Leu	Ser	
			210			215					220					
gaa	gaa	gaa	caa	aaa	ttg	gcg	cgt	ccg	aaa	ctg	ttt	tgg	tgg	aat	gtc	720
Glu	Glu	Glu	Gln	Lys	Leu	Ala	Arg	Pro	Lys	Leu	Phe	Trp	Trp	Asn	Val	
225					230				235					240		
ctg	ctg	ttt	ttg	gcg	gcg	atg	agc	ctg	ctt	ttt	tcg	ggc	acc	ttc	ccg	768
Leu	Leu	Phe	Leu	Ala	Ala	Met	Ser	Leu	Leu	Phe	Ser	Gly	Ile	Phe	Pro	
			245						250					255		
ccg	ggt	tat	gta	ttt	atg	ctg	gct	gca	acg	gcg	gcg	ttg	ctt	ttg	aat	816
Pro	Gly	Tyr	Val	Phe	Met	Leu	Ala	Ala	Thr	Ala	Ala	Leu	Leu	Leu	Asn	
			260					265					270			
tac	cgc	agc	ccg	cag	gaa	cag	atg	gag	cgg	att	tat	gcc	acc	gcc	ggc	864
Tyr	Arg	Ser	Pro	Gln	Glu	Gln	Met	Glu	Arg	Ile	Tyr	Ala	His	Ala	Gly	
		275					280					285				
ggc	gcg	gtg	atg	atg	gcg	tcg	att	att	ttg	gcg	gca	ggc	acg	ttt	ttg	912
Gly	Ala	Val	Met	Met	Ala	Ser	Ile	Ile	Leu	Ala	Ala	Gly	Thr	Phe	Leu	
			290			295					300					
ggg	att	ttg	aag	ggt	gcg	ggg	atg	ttg	gac	gcg	att	ttc	aaa	gac	att	960
Gly	Ile	Leu	Lys	Gly	Ala	Gly	Met	Leu	Asp	Ala	Ile	Ser	Lys	Asp	Ile	
305					310				315					320		
gtg	cat	atc	ctg	ccg	gac	gcg	ctg	ctg	ccg	ctt	ctg	cat	att	gcc	atc	1008
Val	His	Ile	Leu	Pro	Asp	Ala	Leu	Leu	Pro	Tyr	Leu	His	Ile	Ala	Ile	
			325						330					335		
ggt	gtg	ttg	ggc	att	ccg	ctt	gag	ttg	ggt	ttg	agt	acg	gac	gct	tat	1056
Gly	Val	Leu	Gly	Ile	Pro	Leu	Glu	Leu	Val	Leu	Ser	Thr	Asp	Ala	Tyr	
			340					345					350			
tat	ttc	gga	ctg	ttt	ccg											

<221> CDS

<222> (1)..(714)

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<400> 15
atg aat aga ccc aag caa ccc ttc ttc cgt ccc gaa gtc gcc gtt gcc 48
Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala
      1              5              10              15

cgc caa acc agc ctg acg ggt aaa gtg att ctg aca cga cgg ttg tca 96
Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser
      20              25              30

ttt tcc cta tgg acg aca ttt gca tgg ata tct gcg tta ttg att atc 144
Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile
      35              40              45

ctg ttt ttg ata ttt ggt aac tat acg cga aag aca aca gtg gag gga 192
Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly
      50              55              60

caa att tta cct gca tgc ggc gta atc agg gtg tat gca cgg gat acg 240
Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
      65              70              75              80

ggg aca att aca gcg aaa ttc gtg gaa gat gga gaa aag gtt aag gct 288
Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala
      85              90              95

ggc gac aag cta ttt gcg ctt tgc acc tca cgt ttc ggc gca gga gat 336
Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
      100             105             110

agc gtg cag cag cag ttg aaa acg gag gca gtt ttg aag aaa acg ttg 384
Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
      115             120             125

gca gaa cag gaa ctg ggt cgt ctg aag ctg ata cac ggg aat gaa acg 432
Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
      130             135             140             145

cgc agc ctt aaa gca act gtc gaa cgt ttg gaa aac cag aaa ctc cat 480
Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Lys Leu His
      145             150             155             160

att tgc caa cag ata gac ggt cag aaa agg cgc att aga ctt gcg gaa 528
Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
      165             170             175

gaa atg ttg cag aaa tat cgt ttc cta tcc gcc aat gat gca gtg cca 576
Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
      180             185             190

aaa caa gaa atg atg aat gtc aag gca gag ctt tta gag cag aaa gcc 624
Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala
      195             200             205

aaa ctt gat gcc tac cgc cga gaa gaa gtc ggg ctg ctt cag gaa atc 672
Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
      210             215             220

cgc acg cag aat ctg aca ttg gcc agc ctc ccc caa gcg gca tga 717
Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
      225             230             235

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0030453.004601

<210> 16
 <211> 238
 <212> PRT
 <213> Neisseria meningitidis

<400> 16
 Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala
 1 5 10 15
 Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser
 20 25 30
 Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Ile Ile
 35 40 45
 Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly
 50 55 60
 Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
 65 70 75 80
 Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala
 85 90 95
 Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
 100 105 110
 Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
 115 120 125
 Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
 130 135 140
 Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Lys Leu His
 145 150 155 160
 Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
 165 170 175
 Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
 180 185 190
 Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala
 195 200 205
 Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
 210 215 220
 Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
 225 230 235

<210> 17
 <211> 690
 <212> DNA
 <213> Neisseria meningitidis

<210> 18
 <211> 229
 <212> PRT
 <213> *Neisseria meningitidis*

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<400> 18
Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp
 1          5          10          15

Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
          20          25          30

Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
          35          40          45

Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
          50          55          60

Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
          65          70          75          80

Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu
          85          90          95

Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
          100          105          110

Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
          115          120          125

Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
          130          135          140

Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
          145          150          155          160

Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
          165          170          175

Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
          180          185          190

Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
          195          200          205

His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser
          210          215          220

Met Ser Gly Lys Leu
          225
    
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<210> 19
 <211> 1743
 <212> DNA
 <213> *Neisseria meningitidis*

<221> CDS

<222> (1) . . (1740)

atg aaa ttt ttt cct gct cca tgt ctg ttg gtt atc ctg gct gtc ata 48
Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile
1 5 10 15

ccc ctt aaa acc tta gct gcc gat gaa aac gat gca gaa ctt atc cgt 96
Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg
20 25 30

TCC atg cag cgt cag cag cac ata gat gct gaa ttg tta act gat gca 144
Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
35 40 45

aat gtc cgt ttc gag caa cca ttg gag aag aac aat tat gtc ctg agt 192
Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser
50 55 60

gaa gat gaa aca ccg tgt act cgg gta aat tac att agt tta gat gat 240
Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp
65 70 75 80

aag acg gcg cgc aaa ttt tct ttt ctt cct tct gtg ctc atg aaa gaa 288
Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu
85 90 95

aca gct ttt aaa act ggg atg tgt tta ggt tcc aat aat ttg agc agg 336
Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg
100 105 110

cta caa aaa gcc gcg caa cag ata ctg att gtg cgt ggc tac ctc act 384
Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr
115 120 125

tcc caa gct att atc caa cca cag aat atg gat tcc gga att ctg aaa 432
Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys
130 135 140

tta cgg gta tca gca ggc gaa atc agg gat atc cgc tat gaa gaa aaa 480
Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys
145 150 155 160

cgg gat gcg aag tct gcc gag ggc agt att agt gca ttc aat aac aaa 528
 Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys
 165 170 175

ctt ccc tta tat agg aac aaa att ctc aat ctt cgc gat gta gag cag 576

Leu	Pro	Leu	Tyr	Arg	Asn	Lys	Ile	Leu	Asn	Leu	Arg	Asp	Val	Glu	Gln	
180							185			190						
ggc	tgc	gaa	aac	ctg	cgt	cgt	tgc	cgc	agt	gtt	aaa	aca	gat	att	cag	624
Gly	Leu	Glu	Asn	Leu	Arg	Arg	Leu	Pro	Ser	Val	Lys	Thr	Asp	Ile	Gln	
195							200			205						
att	ata	ccg	tcc	gaa	gaa	gaa	ggc	aaa	agc	gat	tta	cag	atc	aaa	tgg	672
Ile	Ile	Pro	Ser	Glu	Glu	Glu	Gly	Lys	Ser	Asp	Leu	Gln	Ile	Lys	Trp	
210							215			220						
cag	cag	aat	aaa	ccc	ata	cgg	ttc	agc	atc	ggc	ata	gat	gat	gcg	ggc	720
Gln	Gln	Asn	Lys	Pro	Ile	Arg	Phe	Ser	Ile	Gly	Ile	Asp	Asp	Ala	Gly	
225							230			235						
ggc	aaa	acg	acc	ggc	aaa	tat	caa	gga	aat	gct	gct	tta	tgc	tcc	gat	768
Gly	Lys	Thr	Thr	Gly	Lys	Tyr	Gln	Gly	Asn	Val	Ala	Leu	Ser	Ser	Asp	
245							250			255						
aac	cct	tgc	ggc	tta	agc	gat	tgc	ttt	tat	gtt	tca	tat	gga	cgc	ggc	816
Asn	Pro	Leu	Gly	Leu	Ser	Asp	Ser	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly	
260							265			270						
tgc	gtg	cac	aaa	acg	gac	tgc	act	cgt	gcc	acc	ggc	acg	gaa	act	gaa	864
Leu	Val	His	Lys	Thr	Asp	Leu	Thr	Ala	Ala	Thr	Gly	Thr	Glu	Thr	Glu	
275							280			285						
agc	gga	tcc	aga	agt	tac	agc	gtg	cat	tat	tgc	gcg	ccc	gta	aaa	aaa	912
Ser	Gly	Ser	Arg	Ser	Tyr	Ser	Val	His	Tyr	Ser	Val	Pro	Val	Lys	Lys	
290							295			300						
tgg	ctg	ttt	tct	ttt	aat	cac	aat	gga	cat	cgt	tac	cac	gaa	gca	acc	960
Trp	Leu	Phe	Ser	Phe	Asn	His	Asn	Gly	His	Arg	Tyr	His	Glu	Ala	Thr	
305							310			315						
gaa	ggc	tat	tcc	gtc	act	tac	gat	tac	aac	ggc	aaa	caa	tat	cag	agc	1008
Glu	Gly	Tyr	Ser	Val	Asn	Tyr	Asp	Tyr	Asn	Gly	Lys	Gln	Tyr	Gln	Ser	
325							330			335						
agc	ctg	gcc	ggc	gag	cgc	atg	ctt	tgg	ccc	ccc	agc	ttt	oct	caa	act	1056
Ser	Leu	Ala	Ala	Glu	Arg	Met	Leu	Trp	Pro	Pro	Ser	Phe	Pro	Gln	Thr	
340							345			350						
tca	gtc	cga	atg	aaa	tta	tgg	aca	cgc	caa	acc	tat	aaa	tac	atc	gac	1104
Ser	Val	Arg	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp	
355							360			365						
gat	gcc	gaa	atc	gaa	gtg	caa	cgc	cgc	cgc	tct	gca	ggc	tgg	gaa	gcc	1152
Asp	Ala	Glu	Ile	Glu	Val	Gln	Arg	Arg	Arg	Ser	Ala	Gly	Trp	Glu	Ala	
370							375			380						
gaa	tgc	cgc	cac	cgt	gct	tac	ctc	cac	cgt	tgg	cag	ctt	gac	ggc	aag	1200
Glu	Leu	Arg	His	Arg	Ala	Tyr	Leu	His	Arg	Trp	Gln	Leu	Asp	Gly	Lys	
385							390			395						
ttg	tct	tac	aaa	cgc	ggg	acc	ggc	atg	cgc	caa	agt	atg	ccc	gca	cct	1248
Leu	Ser	Tyr	Lys	Arg	Gly	Thr	Gly	Met	Arg	Gln	Ser	Met	Pro	Ala	Pro	
405							410			415						
gaa	gaa	aac	ggc	ggc	ggc	act	att	cca	gcc	aca	tcc	cgt	atg	aaa	atc	1296

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<210> 20
<211> 580
<212> PRT
<213> Neisseria meningitidis
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400> 20
Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile
 1 5 10 15

Pro Leu Lys Thr Léu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg
 20 25 30

Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
 35 40 45

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser

50	55	60
Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp		
65	70	75 80
Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu		
	85	90 95
Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg		
	100	105 110
Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr		
	115	120 125
Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys		
	130	135 140
Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys		
	145	150 155 160
Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys		
	165	170 175
Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln		
	180	185 190
Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln		
	195	200 205
Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp		
	210	215 220
Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly		
	225	230 235 240
Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp		
	245	250 255
Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly		
	260	265 270
Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu		
	275	280 285
Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys		
	290	295 300
Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr		
	305	310 315 320
Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser		
	325	330 335
Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr		
	340	345 350
Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp		
	355	360 365
Asp Ala Glu Ile Glu Val Gln Arg Arg Arg Ser Ala Gly Trp Glu Ala		

380

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<220>  
<221> CDS  
<222> (1) .. (408)
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<210> 22
<211> 136
<212> PRT
<213> Neisseria meningitidis
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$\langle 222 \rangle \quad (1) \dots (921)$

400> 23																
atg	caa	tac	agc	aca	ctg	gca	gga	caa	acc	gac	aac	tcc	ctc	gtt	tcc	48
Met	Gln	Tyr	Ser	Thr	Leu	Ala	Gly	Gln	Thr	Asp	Asn	Ser	Leu	Val	Ser	
1 5 10 15																
aat	aat	ttc	ggg	ttt	ttg	cgc	ctg	ccg	ctt	aat	ttt	atg	ccg	tat	gaa	96
Asn	Asn	Phe	Gly	Phe	Leu	Arg	Leu	Pro	Leu	Asn	Phe	Met	Pro	Tyr	Glu	
20 25 30																
agt	cat	gcc	gat	tgg	gtt	att	acc	ggc	gtg	ccc	tat	gat	atg	gcg	gtt	144
Ser	His	Ala	Asp	Trp	Val	Ile	Thr	Gly	Val	Pro	Tyr	Asp	Met	Ala	Val	
35 40 45																
tca	ggg	cgt	tcc	ggc	gcg	cgt	ttc	ggc	ccc	gaa	gcc	atc	cgg	cgc	gcc	192
Ser	Gly	Arg	Ser	Gly	Ala	Arg	Phe	Gly	Pro	Glu	Ala	Ile	Arg	Arg	Ala	
50 55 60																
tcc	gtc	aac	ctc	gct	tgg	gag	cac	cgc	agg	ttt	cca	tgg	aca	ttt	gat	240
Ser	Val	Asn	Leu	Ala	Trp	Glu	His	Arg	Arg	Phe	Pro	Trp	Thr	Phe	Asp	
65 70 75 80																
gtg	cgc	gaa	cgc	ctg	aac	att	att	gat	tgc	ggc	gac	ttg	gtt	ttc	tct	288
Val	Arg	Glu	Arg	Leu	Asn	Ile	Ile	Asp	Cys	Gly	Asp	Leu	Val	Phe	Ser	
85 90 95																
ttt	ggc	gac	agc	agg	gat	ttt	gtc	gaa	aaa	atg	gaa	gcg	cac	gcc	ggc	336
Phe	Gly	Asp	Ser	Arg	Asp	Phe	Val	Glu	Lys	Met	Glu	Ala	His	Ala	Gly	
100 105 110																
aaa	tta	ctt	tct	tcc	ggc	aaa	cgc	tgt	ttg	agt	ttg	ggc	ggc	gac	cat	384
Leu	Leu	Ser	Ser	Ser	Gly	Lys	Arg	Cys	Leu	Ser	Leu	Gly	Gly	Asp	His	
115 120 125																
ttc	att	acc	ctc	ccg	ttg	ttg	cgc	gcc	cac	gcc	cgc	tat	ttc	ggc	aaa	432
Phe	Ile	Thr	Leu	Pro	Leu	Leu	Arg	Ala	His	Ala	Arg	Tyr	Phe	Gly	Lys	
130 135 140																
ctc	gca	ctg	att	cat	ttt	gac	gcg	cac	acc	gac	acc	tac	gac	aac	ggc	480
Leu	Ala	Leu	Ile	His	Phe	Asp	Ala	His	Thr	Asp	Thr	Tyr	Asp	Asn	Gly	
145 150 155 160																
agc	gaa	tac	gac	cac	ggc	acg	atg	ttc	tat	acc	gcc	ccc	aag	gaa	ggc	528
Ser	Glu	Tyr	Asp	His	Gly	Thr	Met	Phe	Tyr	Thr	Ala	Pro	Lys	Glu	Gly	
165 170																
ctc	atc	gac	ccg	tcc	cgt	tcc	ata	caa	atc	ggc	ata	cgt	acc	gaa	cac	576

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
180 185 190

agt aaa aaa ttg cct ttt act gtg ttg acc gcc ccc caa gtt aat gaa 624
Ser Lys Lys Leu Pro Phe Thr Val Leu Thr Ala Pro Gln Val Asn Glu
195 200 205

gac agt gtt gaa gag acc gtc cgt aaa atc aaa gaa acc gtc ggc aat 672
Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
210 215 220

atg ccc gtt tac ctg act ttc gac ata gac tgc ctc gac cgg tgg ttc 720
Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
225 230 235 240

gcc ccc ggg acc ggt acg ccc gta tgc ggc ggc ttg agc agc gac agg 768
Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
245 250 255

gca tta aaa atc cta cgt ggg ctg acg gat ctc gac atc gtc ggt atg 816
Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
260 265 270

gat gtt gta gaa gtt gcc ccc tct tac gac caa tcc gac att acc gct 864
Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
275 280 285

ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg 912
Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
290 295 300

aaa aag gac tga 924
Lys Lys Asp
305

<210> 24
<211> 307
<212> PRT
<213> Neisseria meningitidis

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Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
20 25 30

Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
35 40 45

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
50 55 60

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
65 70 75 80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
85 90 95

<400> 25
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 Met Glu Gln Ser Gly Lys Phe Ser Trp Ser Ala Ala Ala Phe Trp Asp
 1 5 10 15

att ccc tac ccc gtc acc agg cgg att gcc tca agt ttg tat tcg acc 96
 Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr
 20 25 30

gaa tat ttt gtc gta tgc ttt ctg cgt ttg atg cca ctc tct ccg tgt 144
 Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys
 35 40 45

aat ctg tat ttt gtc acc cat ctg cgt acc aat gaa tcg gaa ata gaa 192
 Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
 50 55 60

aga tgg tct gct gtt ccc tgc caa ata gta ttg aac gac ggc aag tcg 240
 Arg Trp Ser Ala Val Pro Cys Glu Ile Val Leu Asn Asp Gly Lys Ser
 65 70 75 80

gaa ttc ggc gga ttc gca ttt gaa gtg caa ctt tcc cta aca gaa aaa 288
 Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
 85 90 95

ggc cag tat gcg gta gca tac gac ctt tcc tgc aag aaa gat tgc cat 336
 Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
 100 105 110

gag cta cac gca act gac cca agg cga acg ata cca cat cca ata cct 384
 Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
 115 120 125

gtc ccg cca ctg cac cgt cac cga aat cgc caa aca gct taa 426
 Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala
 130 135 140

<210> 26

<211> 141

<212> PRT

<213> Neisseria meningitidis

Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
35 40 45

Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
50 55 60

Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
65 70 75 80

Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
85 90 95

His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
100 105 110

Leu Arg Arg His
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<210> 29
<211> 1404
<212> DNA
<213> Neisseria meningitidis

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<222> (1)..(1401)

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Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
1 5 10 15

tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tgg gct atg 96
Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
20 25 30

aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144
Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
35 40 45

cca cta tcc ctt tcc cca tcc gtt tgg gct ttt acg ctg cct gaa gca 192
Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
50 55 60

tgg cgg gcg gcg cag caa cat tgg gct gat ttt caa gcg tcc cat tac 240
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
65 70 75 80

cag cgt gat gca gtg cgc gca cgg caa caa gcc aag gcc gca ttc 288
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
85 90 95

ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag cgg cca tgg 336
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
100 105 110

att tct tcc acc cgc gaa aca cag gga tgg agc gtg cag gtg gga caa 384

SECRET

Ile	Ser	Ser	Thr	Arg	Glu	Thr	Gln	Gly	Trp	Ser	Val	Gln	Val	Gly	Gln	
115							120				125					
acc	tta	ttt	gac	gct	gcc	aaa	ttt	gca	caa	tac	cgc	caa	agc	agg	ttc	432
Thr	Leu	Phe	Asp	Ala	Ala	Lys	Phe	Ala	Gln	Tyr	Arg	Gln	Ser	Arg	Phe	
130						135					140					
gat	acg	cag	gct	gca	gaa	cag	cgt	ttc	gat	gcg	gca	cgc	gaa	gaa	ttg	480
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu	
145					150					155					160	
ctg	ttg	aaa	gtt	gcc	gaa	agt	tat	ttc	aac	gtt	tta	ctc	agc	cga	gac	528
Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp	
				165					170					175		
acc	gtt	gcc	gcc	cat	gcg	gcg	gaa	aaa	gag	gct	tat	gcc	cag	cag	gta	576
Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val	
				180				185					190			
agg	cag	gcg	gcg	gct	tta	ttc	aat	aaa	ggt	gct	gcc	acc	gcg	ctg	gat	624
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp	
				195			200					205				
att	cac	gaa	gcc	aaa	gcc	ggt	tac	gac	aat	gcc	ctg	gcc	caa	gaa	atc	672
Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile	
210					215					220						
gcc	gta	ttg	gct	gag	aaa	caa	acc	tat	gaa	aac	cag	ttg	aac	gac	tac	720
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr	
225				230					235					240		
acc	gac	ctg	gat	agc	aaa	caa	atc	gag	gcc	ata	gat	acc	gcc	aac	ctg	768
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu	
				245				250						255		
ttg	gca	cgc	tat	ctg	ccc	aag	ctg	gaa	cgt	tac	agt	ctg	gat	gaa	tgg	816
Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp	
			260				265						270			
cag	cgc	att	gcc	tta	tcc	aac	aat	cat	gaa	tac	cgg	atg	cag	cag	ctt	864
Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu	
275							280				285					
gcc	ctg	caa	agc	agc	gga	cag	gcg	ctt	cgg	gca	gca	cag	aac	agc	cgc	912
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Gln	Asn	Ser	Arg	
290						295				300						
tat	ccc	acc	gtt	tct	gcc	cat	gtc	ggc	tat	cag	aat	aac	ctc	tac	act	960
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Thr	
305					310				315					320		
tca	tct	gcg	cag	aat	aat	gac	tac	cac	tat	cgg	ggc	aaa	ggg</			

115					120					125					
Thr	Leu	Phe	Asp	Ala	Ala	Lys	Phe	Ala	Gln	Tyr	Arg	Gln	Ser	Arg	Phe
130					135					140					
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu
145					150					155					160
Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp
					165					170				175	
Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val
					180					185				190	
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp
					195			200				205			
Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile
					210			215				220			
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr
					225					235					240
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu
					245					250				255	
Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp
					260					265				270	
Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu
					275			280				285			
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Cln	Asn	Ser	Arg
					290			295				300			
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Trp
					310					315					320
Ser	Ser	Ala	Gln	Asn	Asn	Asp	Tyr	His	Tyr	Arg	Gly	Lys	Gly	Met	Ser
					325					330				335	
Val	Gly	Val	Gln	Leu	Asn	Leu	Pro	Leu	Tyr	Thr	Gly	Gly	Glu	Leu	Ser
					340					345				350	
Gly	Lys	Ile	His	Glu	Ala	Glu	Ala	Gln	Tyr	Gly	Ala	Ala	Glu	Ala	Gln
					355			360				365			
Leu	Thr	Ala	Thr	Glu	Arg	His	Ile	Lys	Leu	Ala	Val	Arg	Gln	Ala	Tyr
					370			375				380			
Thr	Glu	Ser	Gly	Ala	Ala	Arg	Tyr	Gln	Ile	Met	Ala	Gln	Glu	Arg	Val
					385					395					400
Leu	Glu	Ser	Ser	Arg	Leu	Lys	Leu	Lys	Ser	Thr	Glu	Thr	Gly	Gln	Gln
					405					410				415	
Tyr	Gly	Ile	Arg	Asn	Arg	Leu	Glu	Val	Ile	Arg	Ala	Arg	Gln	Glu	Val
					420			425						430	
Ala	Gln	Ala	Glu	Gln	Lys	Leu	Ala	Gln	Ala	Arg	Tyr	Lys	Phe	Met	Leu

435

440

445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

Phe Ala Glu
465

<210> 31
<211> 696
<212> DNA
<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(693)

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aca ttg ggc att tgc cgg ctt tta gcc ttt tgt ttt ggc cgg gcc atc 96
Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
20 25 30
gca tca ggt tat cac tgg gaa tat gaa tac ggc tac cgt tat tct gcc 144
Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
35 40 45
gtg ggt gct ttg gct tgg gtt gta ttt tta tta tta ttg gca cgt ggt 192
Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
50 55 60
ttc cgg cgc gtt tct tca gtc gtt tta ctg att tac gtc ggc aca acc 240
Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
65 70 75 80
gcc cta tat ttg cgg gtc gcc tgg ctg tat ggt ggc cgg tct tat cag 288
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
85 90 95
ata gtc ggt tgg ata ttg gaa agc aat ctt gcc gag cgg cgt gaa ttt 336
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
100 105 110
gtc ggc aat ctt ccc ggg tgg ctt tat ttt gtg cag gca tta ttt ttc 384
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
115 120 125
att ttt ggc ttg aca gtt tgg aga tat tgt gta tgg ggg ggg gta ttt 432
Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe
130 135 140
gct gac gta aaa aac tat aaa cgc cgt agc aaa ata tgg ctg act ata 480
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
145 150 155 160

09030473.001604

tta ttg act ttg att ttg tcc tgc gcg gtg atg gat aaa atc gcc agc	528
Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser	
165 170 175	
gat aaa gat ttg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc	576
Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe	
180 185 190	
gac ctg tat tac gat ttg gct tcc gcg ccg gca cca ata tgt cgc caa	624
Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln	
195 200 205	
gcg cgc cca cat ttt gga agc agc aaa aaa agc gtc aac atg gca tat	672
Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr	
210 215 220	
ccg tca tgt tgc gcc caa gta taa	696
Pro Ser Cys Cys Ala Gln Val	
225 230	

<210> 32
 <211> 231
 <212> PRT
 <213> Neisseria meningitidis

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 Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
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 Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
 35 40 45
 Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Ala Arg Gly
 50 55 60
 Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
 65 70 75 80
 Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
 85 90 95
 Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
 100 105 110
 Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
 115 120 125
 Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe
 130 135 140
 Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
 145 150 155 160
 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser
 165 170 175

Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe 180 185 190
 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln 195 200 205
 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr 210 215 220
 Pro Ser Cys Cys Ala Gln Val 225 230

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 <211> 909
 <212> DNA
 <213> Neisseria meningitidis

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 <221> CDS
 <222> (1)..(906)

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 Met Asn Val Tyr Gly Phe Pro Leu Pro Asp Thr Pro Phe Leu Ser Arg
 1 5 10 15
 acc aaa ggg ctg ttg ata aac ggt tac cat ttc acc gcc cac ggc acg 96
 Thr Lys Gly Leu Leu Ile Asn Gly Tyr His Phe Thr Ala His Ala Thr
 20 25 30
 aat ctt ttg ctg cgg cag act ttg ggg ctg cgg gga gag cgg aac aat 144
 Asn Leu Ser Leu Pro Gln Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn
 35 40 45
 aac att gtc agc ttg ggc aag cag ggc ggt ttt cgg acg ggg tgg ctg 192
 Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu
 50 55 60
 tct aat caa gga atg ttg ggg cat ttt gcc aac gaa att tcc acc tat 240
 Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr
 65 70 75 80
 gcc cta cgc agc gat tat cgg tgg ttt acc caa agg ggt gat tat ggc 288
 Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly
 85 90 95
 aaa agc ggc ggg ttg agc gat cgc ctt ttg ttg cgg ggc ttc aaa cgg 336
 Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Pro Ala Phe Lys Arg
 100 105 110
 gct ttg ata gga aat gca ggc acg aag cct cgg ctg att gtg atg cac 384
 Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His
 115 120 125
 ctg atg ggt ttg cac agt gat ttt tgc aca cgt ttg gat aag gat ggc 432
 Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala
 130 135 140

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<210> 34
<211> 302
<212> PRT
<213> Neisseria meningitidis
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Thr Lys Gly Leu Leu Ile Asn Gly Tyr His Phe Thr Ala His Ala Thr
          20          25          30
Asn Leu Ser Leu Pro Gln Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn
  35          40          45
Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu
  50          55          60
Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr

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65	70	75	98
Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly 85 90 95			
Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Pro Ala Phe Lys Arg 100 105 110			
Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His 115 120 125			
Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala 130 135 140			
Arg Arg Phe Gln Tyr Gln Thr Glu Lys Ile Ser Cys Tyr Val Ser Thr 145 150 155			
Ile Ala Gln Thr Asp Lys Phe Leu Glu Asp Thr Val Lys Ile Leu Asn 165 170 175			
Glu Asn Lys Gly Ser Trp Ser Leu Val Tyr Phe Ser Asp His Gly Leu 180 185 190			
Met His Val Gly Lys Gly Gly Glu Arg Thr Leu Thr His Gly Ala Trp 195 200 205			
Lys Arg Gln Ser Tyr Gly Val Pro Leu Val Lys Ile Ser Ser Asp Asp 210 215 220			
Thr Arg Arg Glu Met Ile Lys Val Arg Arg Ser Ala Phe Asn Phe Leu 225 230 235			
Arg Gly Phe Gly Ser Trp Tar Gly Ile Glu Thr Asp Glu Leu Pro Asp 245 250 255			
Asp Gly Tyr Asp Phe Trp Gly Asn Val Pro Asp Val Gln Gly Glu Gly 260 265 270			
Asn Asn Leu Ala Phe Ile Asp Gly Leu Pro Asp Asp Pro Ala Pro Trp 275 280 285			
Tyr Ala Gly Lys Gly Lys Ser Thr Lys Asn Thr Ser Lys Lys 290 295 300			

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<212> DNA
<213> Neisseria meningitidis
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<221> CDS
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gaa tgc aat cgc ctt gcc gtc gcc ggt tgc gtc aat gct tat ttt gca 96
Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala
20 25 30

cga ttg gcc acc caa agc ggt ttc aaa gcc atc tat ctg tcc ggc ggc 144
Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly
35 40 45

ggc gtg gca gcc tgt tct tgc ggt atc cct gat ttg ggc att acc aca 192
Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr
50 55 60

atg gaa gat gtg ctg atc gac gca cga cgc att acg gac aac gtg gat 240
Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp
65 70 75 80

acg cct ctg ctg gtg gac atc gat gtg ggt tgg ggc ggt gca ttc aat 288
Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn
85 90 95

att gcc cgt acc att cgc aac ttt gaa cgc gcc ggt gtt gca ggc gtt 336
Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val
100 105 110

cac atc gaa gat cag gta gcg caa aaa cgt tgc ggc cac cgt cgc aac 384
His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn
115 120 125

aaa gcc att gta tct aaa gat gaa atg gtc gac cgt atc aaa gct gcc 432
Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala
130 135 140

gta gat gcg cgc gtt gat gag aac ttc gtg att atg gcg cgt acc gat 480
Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp
145 150 155 160

ggc ctg gcg gta gaa ggt ttg gat gcc gct acc gaa cgc gcc caa gct 528
Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala
165 170 175

tgt gtc gaa gcc ggt gcg gac atg att ttc cct gaa gcc atg acc gat 576
Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp
180 185 190

ttg aac atg tac cgc caa ttt gca gat gcg gtg aaa gtg ccc gtg ttg 624
Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu
195 200 205

ggc aac att acc gag tct ggt tcc acc cgc ctt tat acc caa agc gag 672
Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu
210 215 220

ctg gct gaa aac ggc gtg ttg ctg gtc cgc tat cgc ctg tca tgc ttc 720
Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe
225 230 235 240

cgt gca gca agc aaa gcc gct ctg aat gtt tac gaa gcg att atg cgc 768
Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg
245 250 255

gat ggc act tca ggc ggc ggt ggt gga cag tat gca aac cag tgc cga 816
Asp Gly Thr Ser Gly Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg
260 265 270

gct gta cga gca tct gaa cta tca tgc ctt cga gca aaa act gga taa 864
Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
275 280 285

<210> 36

<211> 287

<212> PRT

<213> Neisseria meningitidis

<400> 36

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20 25 30

Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly
35 40 45

Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr
50 55 60

Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp
65 70 75 80

Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn
85 90 95

Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Val
100 105 110

His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn
115 120 125

Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala
130 135 140

Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp
145 150 155 160

Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala
165 170 175

Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp
180 185 190

Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu
195 200 205

Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu
210 215 220

Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe
225 230 235 240

Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg
245 250 255

Asp Gly Thr Ser Gly Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg
260 265 270

Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
275 280 285

<210> 37

<211> 921

<212> DNA

<213> *Neisseria meningitidis*

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<221> CDS

<222> (1) .. (918)

<400> 37

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 5 10 15

[illegible]

AAA CCC ATA AAA ACA GAA AGG AGA AAT ACC ATG ACT GAA ACT ACC GAA 144
Lys Pro Ile Lys Thr Gln Arg Arg Ser Thr Met Thr Glu Thr Thr Gln
25 46 45

600
Thr Thr Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala 192

80 60

gga ggt aac aac ggt tgg tgt acc gta ggc ggt acc ggc aac gat ttg 240
ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu
65 70 75 80

aga tat cgc ggt tac gac att arg gag ttc gca caa aaa tgg gag ttt 286
Ser Tyr Arg Gly Tyr Asp Ile Leu Arg Leu Ala Gln Lys Cys Glu Phe

85 90 95

GAA GAG GAT GGC GAC GGG GGG GAT GAG GGG GAT TTA GCG AAG AAA TTT 336
Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe
100 336 336

gag ctg gcc gct taa aaa gcc aag ctg aaa tcc atg cgc gcc ctg cct 384
 Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro
 115 120 125

atc cgt gtc att aaa gtt ttg gaa agc ctg cct gca cat acc cat ccg 432
ile arg val ile lys val leu glu ser leu pro ala his thr his pro
130 135 140

atg gac gtg atg cgt acc ggc gta tcc atg ctg ggc tgt gtt cat cct 480
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<210> 38
<211> 306
<212> PRT
<213> Neisseria meningitidis
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<400> 38
Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro
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Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro
      20              25              30
Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Gln Thr Thr Gln
      35              40              45
Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala
      50              55              60

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Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu
65 70 75 80

Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe
85 90 95

Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe
100 105 110

Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro
115 120 125

Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro
130 135 140

Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro
145 150 155 160

Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys
165 170 175

Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser
180 185 190

His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Glu Thr Ile Gly
195 200 205

Gly His Phe Leu His Leu Leu His Gly Lys Arg Pro Ser Glu Ser His
210 215 220

Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe
225 230 235 240

Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp
245 250 255

Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys
260 265 270

His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala
275 280 285

Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys
290 295 300

Lys Ser
305

<210> 39
<211> 945
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(942)

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1	5			5				10					15			
tta	ctg	atg	gga	aaa	ttc	ttg	gca	gtt	tct	gcg	gcc	ctt	ctg	aat	gca	95
Leu	Leu	Met	Gly	Ile	Phe	Leu	Ala	Val	Ser	Ala	Ala	Leu	Leu	Asn	Ala	
			20				25					30				
acc	atc	ggc	ata	ttc	agc	aag	ata	ttg	atg	gag	cag	ggc	ttg	tct	ggt	144
Thr	Ile	Gly	Ile	Phe	Ser	Lys	Ile	Leu	Met	Glu	Gln	Gly	Leu	Ser	Val	
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cag	cat	att	gca	ttt	ttg	aaa	act	ttg	aca	ggt	ttc	gtg	ttt	atc	agc	192
Gln	His	Ile	Ala	Phe	Leu	Lys	Thr	Leu	Thr	Gly	Phe	Val	Phe	Ile	Ser	
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att	ttg	ctt	tgc	cgt	acc	ggt	ttt	acc	aga	cag	att	gcg	gat	att	tca	240
Ile	Leu	Leu	Cys	Arg	Thr	Gly	Phe	Thr	Arg	Gln	Ile	Ala	Asp	Ile	Ser	
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aga	aag	aaa	gag	gca	att	ttg	ccg	ttg	ctg	tta	aaa	gta	gca	att	tgt	288
Arg	Lys	Lys	Glu	Ala	Ile	Leu	Pro	Leu	Leu	Leu	Lys	Val	Ala	Ile	Cys	
				85					90					95		
gct	ttt	ttc	gga	att	tat	acg	ttg	ttt	ttc	ttt	gaa	acc	aca	gct	tat	336
Ala	Phe	Phe	Gly	Ile	Tyr	Thr	Leu	Phe	Phe	Phe	Glu	Thr	Thr	Ala	Tyr	
			100					105					110			
caa	tat	ggc	aat	gct	gcg	aat	gta	gta	gtt	gta	tta	atg	gca	tcg	gct	384
Gln	Tyr	Gly	Asn	Ala	Ala	Asn	Val	Val	Val	Val	Leu	Met	Ala	Ser	Ala	
		115				120						125				
gcc	gta	tct	gcc	ttg	ata	ttg	gac	agc	ata	ctg	tta	gat	gaa	cgt	att	432
Ala	Val	Ser	Ala	Leu	Ile	Leu	Asp	Ser	Ile	Leu	Leu	Asp	Glu	Arg	Ile	
	130				135						140					
tgc	att	tct	tca	gtc	gtc	ggt	gtg	ggt	ttg	gca	gta	ttg	ggg	atc	gca	480
Cys	Ile	Ser	Ser	Val	Val	Gly	Val	Gly	Leu	Ala	Val	Leu	Gly	Ile	Ala	
145				150					155					160		
atg	att	tct	tgg	act	gga	gaa	gga	agt	tta	ggg	ttg	att	ctg	aat	gcc	528
Met	Ile	Ser	Trp	Thr	Gly	Glu	Gly	Ser	Leu	Gly	Leu	Ile	Leu	Asn	Ala	
			165						170					175		
gca	ctg	gcg	ggc	tcg	ggc	tac	ggt	tgt	ttt	tcc	gtt	ttg	att	aag	aaa	576
Ala	Leu	Ala	Gly	Ser	Gly	Tyr	Gly	Cys	Phe	Ser	Val	Leu	Ile	Lys	Lys	
			180					185					190			
ttc	ggc	cta	aac	ggc	ggt	att	tat	ttg	aca	cgg	ata	ttg	atg	ttt	ttt	624
Phe	Gly	Leu	Asn	Gly	Gly	Ile	Tyr	Leu	Thr	Arg	Ile	Leu	Met	Phe	Phe	
		195					200					205				

ccg acg att tta gga ttt tat tgt aca act aaa gca ttg gat tat ttg 768
Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu
245 250 255

agt gct cgg aag gta cag gta act gaa ttg gcc gag cca ttg ttt gct 816
Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala
260 265 270

gcc gta ctg gct tgg ttg ttt ttg aat gaa ata ccg gaa gga cgc ttc 864
Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe
275 280 285

ttt gtc ggc gcc att ctg att att gcc ggt att gtg tct atc aat ggg 912
Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly
290 295 300

ctg tat cga cca ttg ttg aag cga att gaa taa 945
Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu
305 310

<210> 40

<211> 314

<212> PRT

<213> Neisseria meningitidis

<400> 40

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20 25 30

Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val
35 40 45

Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser
50 55 60

Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser
65 70 75 80

Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Lys Val Ala Ile Cys
85 90 95

Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr
100 105 110

Gln Tyr Gly Asn Ala Ala Asn Val Val Val Leu Met Ala Ser Ala
115 120 125

Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile
130 135 140

Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala
145 150 155 160

Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala
165 170 175

Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys
180 185 190

Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe
195 200 205

Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile
210 215 220

His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu
225 230 235 240

Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu
245 250 255

Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala
260 265 270

Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe
275 280 285

Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly
290 295 300

Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu
305 310

<210> 41
<211> 2610
<212> DNA
<213> Neisseria meningitidis

<220>
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<222> (1)..(2607)

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gaa tac tac gac gcg cgt gcg gcg tgt gag gac atc aag ccc ggc tct 96
Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser
20 25 30

tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144
Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
35 40 45

aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192
Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
50 55 60

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg 240
Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
65 70 75 80

cgg gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg 288

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu	
85 90 95	
gca ggt ctg cgc gat gcg att gcc gaa aaa ggc ggc gat cct gcc aaa	336
Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys	
100 105 110	
gtg aat ccg gtg gtt gca aaa ccc agc ttc atc gtc gac cac tct ctg	384
Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu	
115 120 125	
gcc gtt gaa tgc ggc ggc tac gac ccc gat gcc ttc cgc aaa aac cgc	432
Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg	
130 135 140	
caa atc gaa gac aga cgt aac gaa gac cgt ttc cac ttc atc aac tgg	480
Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp	
145 150 155 160	
aca aaa acc gca ttt gaa aat gtg gac gtg att ccg gcg ggc aac ggc	528
Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly	
165 170 175	
atc atg cac caa atc aat cta gaa aaa atg tgc ccc gtc gtc caa gtc	576
Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val	
180 185 190	
aaa aac ggc gtg gcg ttc ccc gat acc tgc gtc ggc acg gat tgc cac	624
Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His	
195 200 205	
acg ccg cac gtc gat gcg ctg ggc gtg att tcc gtg ggc gtg ggc gga	672
Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly	
210 215 220	
ttg gaa gcg gaa acc gtg atg ctg ggt cgc gcg tcc atg atg cgc ctg	720
Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu	
225 230 235 240	
ccc gat att gtc ggc gtt gag ctg aac ggc aaa cgg cag gcg ggc att	768
Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile	
245 250 255	
acg gcg acg gat att gtg ttg gca ctg acc gag ttt ctg cgc aaa gaa	816
Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu	
260 265 270	
cgc gtg gtc ggg gcg ttt gtc gaa ttc ttc ggc gag ggc gcg aga agc	864
Arg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser	
275 280 285	
ctg tct atc ggc gac cgc gcg acc att tcc aac atg acg ccg gag ttc	912
Leu Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe	
290 295 300	
ggc gcg act gcc gcg atg ttc gct att gat gag caa acc att gat tat	960
Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr	
305 310 315 320	
ttg aaa ctg acc gga cgc gac gac gcg cag gtg aaa ttg gtg gaa acc	1008

Leu Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr	
325 330 335	
tac gcc aaa acc gca ggc tta tgg gca gat gcc ttg aaa acc gcc gtc	1056
Tyr Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val	
340 345 350	
tat ccg cgc gtt ttg aaa ttt gat ttg agc agc gta acg cgc aat atg	1104
Tyr Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met	
355 360 365	
gca ggc ccg agc aac ccg cac gcg cgt ttt gcg acc gcc gat ttg gcc	1152
Ala Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala	
370 375 380	
agc aaa ggc ttg gct aaa cct tac gaa gag cct tca gac gcc caa atg	1200
Ser Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met	
385 390 395 400	
ccc gac ggc gcg gtc atc atc gcc gcg att acc agt tgc acc aac act	1248
Pro Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr	
405 410 415	
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Ser Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala	
420 425 430	
aac tgc ttc ggg ctg aaa cgc aaa ccg tgg gtc aaa acc tgc ttt gcc	1344
Asn Cys Phe Gly Leu Lys Arg Lys Pro Trp Val Lys Thr Ser Phe Ala	
435 440 445	
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Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Gly Leu Leu	
450 455 460	
ccc gaa atg gaa aaa ctc ggc ttc ggt atc gtc gcc ttc gcc tgc acc	1440
Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr	
465 470 475 480	
acc tgc aac ggc atg agt ggc gcg ctg gat ccg aaa atc cag aaa gaa	1488
Thr Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu	
485 490 495	
atc atc gac cgc gat ttg tac gcc acc gcc gta tta tca gcc aac cgc	1536
Ile Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg	
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aac ttc gac ggc cgt gtc cat ccg tat gcg aaa cag gct ttc ctc gct	1584
Asn Phe Asp Gly Arg Val His Pro Tyr Ala Lys Gln Ala Phe Leu Ala	
515 520 525	
tcg cct ccg ttg gtc gtt gcc tac gcg ctg gca ggc agt atc cgt ttc	1632
Ser Pro Pro Leu Val Val Tyr Tyr Ala Leu Ala Gly Ser Ile Arg Phe	
530 535 540	
gat att gaa aac gac gta ctc ggc gtt gca gac gcc aag gaa atc cgc	1680
Asp Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg	
545 550 555 560	
ctg aaa gac att tgg cct gcc gat gaa gaa atc gat gcc gtc gtt gcc	1728

Leu	Lys	Asp	Ile	Trp	Pro	Ala	Asp	Glu	Glu	Ile	Asp	Ala	Val	Val	Ala	
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gaa	tat	gtg	aaa	cgc	cag	cgc	tac	cgc	gat	gtg	tat	gta	ccg	atg	ttc	1776
Glu	Tyr	Val	580	Pro	Gln	Gln	Phe	Arg	Asp	Val	Tyr	Val	590	Met	Phe	
gac	acc	ggc	aca	cgc	caa	aaa	gca	cct	agt	ccg	ctg	tac	gat	tgg	cgc	1824
Asp	Thr	Gly	Thr	Ala	Gln	Lys	Ala	Pro	Ser	Pro	Leu	Tyr	Asp	Trp	Arg	
		595					600					605				
ccg	atg	tcc	acc	tac	atc	cgc	cgt	ccg	cct	tac	tgg	gaa	ggc	cgc	ctg	1872
Pro	Met	Ser	Ser	Thr	Tyr	Ile	Arg	Arg	Pro	Pro	Tyr	Trp	Glu	Gly	Ala	Leu
		610				615					620					
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Ala	Gly	Glu	Arg	Thr	Leu	Arg	Gly	Met	Arg	Pro	Leu	Ala	Ile	Leu	Pro	
625					630					635					640	
gac	aar	atc	acc	acc	gac	cac	ctc	tcg	ccg	tcc	aat	cgc	att	tgg	gcc	1968
Asp	Asn	Ile	Thr	Thr	Asp	His	Leu	Ser	Pro	Ser	Asn	Ala	Ile	Leu	Ala	
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gtc	agt	gcc	gca	ggc	gag	tat	ttg	gcg	aaa	atg	ggc	ttg	cct	gaa	gaa	2016
Val	Ser	Ala	Ala	Gly	Glu	Tyr	Leu	Ala	Lys	Met	Gly	Leu	Pro	Glu	Glu	
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gac	ttc	aac	tct	tac	gca	acc	cac	cgc	ggc	gac	cac	ttg	acc	gcc	caa	2064
Asp	Phe	Asn	Ser	Tyr	Ala	Thr	His	Arg	Gly	Asp	His	Leu	Thr	Ala	Gln	
				675			680					685				
cgc	gct	acc	ttc	gcc	aat	ccg	aaa	ctg	ttt	aac	gaa	atg	gtg	aaa	aac	2112
Arg	Ala	Thr	Phe	Ala	Asn	Pro	Lys	Leu	Phe	Asn	Glu	Met	Val	Lys	Asn	
				690			695				700					
gaa	gac	ggc	agc	gtg	cgc	caa	ggc	tcg	ttc	gcc	cgc	gtc	gaa	ccc	gaa	2160
Glu	Asp	Gly	Ser	Val	Arg	Gln	Gly	Ser	Phe	Ala	Arg	Val	Glu	Pro	Glu	
705					710					715					720	
ggc	gaa	acc	atg	cgc	atg	tgg	gaa	gcc	atc	gaa	acc	tat	atg	aac	cgc	2208
Gly	Glu	Thr	Met	Arg	Met	Trp	Glu	Ala	Ile	Glu	Thr	Tyr	Met	Asn	Arg	
				725					730					735		
aaa	cag	ccg	ctc	atc	atc	att	gcc	ggt	gcg	gac	tat	ggc	caa	ggc	tca	2256
Lys	Gln	Pro	Leu	Ile	Ile	Ile	Ala	Gly	Ala	Asp	Tyr	Gly	Gln	Gly	Ser	
				740				745				750				
agc	cgc	gac	tgg	gct	gca	aaa	ggc	cta	cgc	ctc	gcc	ggc	gta	gaa	gcg	2304
Ser	Arg	Asp	Trp	Ala	Ala	Lys	Gly	Val	Arg	Ile	Leu	Ala	Gly	Glu	Ala	
				755			760					765				
att	gtt	gcc	gaa	ggc	ttc	gag	cgt	atc	cac	cgc	acc	aac	ctt	atc	ggc	2352
Ile	Val	Ala	Glu	Gly	Phe	Glu	Arg	Ile	His	Arg	Thr	Asn	Leu	Ile	Gly	
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[illegible]

<210> 42

<211> 869

<212> PRT

<213> *Neisseria meningitidis*

<400> 42

Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu
1 5 10 15

Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser
20 25 30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
35 40 45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
50 55 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
65 70 75 80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
85 90 95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
100 105 110

Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu
115 120 125

Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg
130 135 140

Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp
145 150 155 160

Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly
165 170 175

Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val

180										185										190													
Lys	Asn	Gly	Val	Ala	Phe	Pro	Asp	Thr	Cys	Val	Gly	Thr	Asp	Ser	His	Lys	Asn	Gly	Val	Ala	Phe	Pro	Asp	Thr	Cys	Val	Gly	Thr	Asp	Ser	His		
	195						200						205										210										
Thr	Pro	His	Val	Asp	Ala	Leu	Gly	Val	Ile	Ser	Val	Gly	Val	Gly	Gly	Thr	Pro	His	Val	Asp	Ala	Leu	Gly	Val	Ile	Ser	Val	Gly	Val	Gly	Gly		
	210						215					220											225										
Leu	Glu	Ala	Glu	Thr	Val	Met	Leu	Gly	Arg	Ala	Ser	Met	Met	Arg	Leu	Leu	Glu	Ala	Glu	Thr	Val	Met	Leu	Gly	Arg	Ala	Ser	Met	Met	Arg	Leu		
	225				230					235					240								245										
Pro	Asp	Ile	Val	Gly	Val	Glu	Leu	Asn	Gly	Lys	Arg	Gln	Ala	Gly	Ile	Pro	Asp	Ile	Val	Gly	Val	Glu	Leu	Asn	Gly	Lys	Arg	Gln	Ala	Gly	Ile		
			245					250						255									255										
Thr	Ala	Thr	Asp	Ile	Val	Leu	Ala	Leu	Thr	Glu	Phe	Leu	Arg	Lys	Glu	Thr	Ala	Thr	Asp	Ile	Val	Leu	Ala	Leu	Thr	Glu	Phe	Leu	Arg	Lys	Glu		
			260					265					270										265										
Arg	Val	Val	Gly	Ala	Phe	Val	Glu	Phe	Phe	Gly	Glu	Gly	Ala	Arg	Ser	Arg	Val	Val	Gly	Ala	Phe	Val	Glu	Phe	Phe	Gly	Glu	Gly	Ala	Arg	Ser		
			275				280					285											275										
Leu	Ser	Ile	Gly	Asp	Arg	Ala	Thr	Ile	Ser	Asn	Met	Thr	Pro	Thr	Glu	Phe	Leu	Ser	Ile	Gly	Asp	Arg	Ala	Thr	Ile	Ser	Asn	Met	Thr	Pro	Thr	Glu	Phe
	290					295					300												290										
Gly	Ala	Thr	Ala	Ala	Met	Phe	Ala	Ile	Asp	Glu	Gln	Thr	Ile	Asp	Tyr	Gly	Ala	Thr	Ala	Ala	Met	Phe	Ala	Ile	Asp	Glu	Gln	Thr	Ile	Asp	Tyr		
	305				310					315				320									305										
Leu	Lys	Leu	Thr	Gly	Arg	Asp	Asp	Ala	Gln	Val	Lys	Leu	Val	Glu	Thr	Leu	Lys	Leu	Thr	Gly	Arg	Asp	Asp	Ala	Gln	Val	Lys	Leu	Val	Glu	Thr		
			325					330					335										325										
Tyr	Ala	Lys	Thr	Ala	Gly	Leu	Trp	Ala	Asp	Ala	Leu	Lys	Thr	Ala	Val	Tyr	Ala	Lys	Thr	Ala	Gly	Leu	Trp	Ala	Asp	Ala	Leu	Lys	Thr	Ala	Val		
			340					345					350										340										
Tyr	Pro	Arg	Val	Leu	Lys	Phe	Asp	Leu	Ser	Ser	Val	Thr	Arg	Asn	Met	Tyr	Pro	Arg	Val	Leu	Lys	Phe	Asp	Leu	Ser	Ser	Val	Thr	Arg	Asn	Met		
		355				360					365												355										
Ala	Gly	Pro	S																														

500	505	510
Asn Phe Asp Gly Arg Val His	Pro Tyr Ala Lys Gln Ala Phe Leu Ala	
515	520	525
Ser Pro Pro Leu Val Val Ala Tyr	Ala Leu Ala Gly Ser Ile Arg Phe	
530	535	540
Asp Ile Glu Asn Asp Val Leu Gly Val Ala	Asp Gly Lys Glu Ile Arg	
545	550	555
Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Val Ala		
565	570	575
Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe		
580	585	590
Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Thr Arg		
595	600	605
Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu		
610	615	620
Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro		
625	630	635
Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala		
645	650	655
Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu		
660	665	670
Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln		
675	680	685
Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn		
690	695	700
Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu		
705	710	715
Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg		
725	730	735
Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser		
740	745	750
Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala		
755	760	765
Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly		
770	775	780
Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr		
785	790	795
Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr		
805	810	815
Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr		

820

825

830

Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu
835 840 845

Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu
850 855 860

Glu Gly Asn Ala Ala
865

<210> 43

<211> 1170

<212> DNA

<213> *Neisseria meningitidis*

$\langle 220 \rangle$

<221> CDS

<222> (1) . . (1167)

400> 43																									
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Met	Pro	Gln	Ile	Lys	Ile	Pro	Ala	Val	Tyr	Tyr	Arg	Gly	Gly	Thr	Ser										
																	1								
																	5								
																	10								
																	15								
aaa ggc gtg ttt ttc aaa cgt tcc gac ctg ccc gag gcg gcg cgg gaa 96																									
Lys	Gly	Val	Phe	Phe	Lys	Arg	Ser	Asp	Leu	Pro	Glu	Ala	Ala	Arg	Glu										
																	20								
																	25								
																	30								
cgc gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc gcc agc ccg 144																									
Ala	Gly	Ser	Ala	Arg	Asp	Lys	Ile	Leu	Leu	Arg	Val	Leu	Gly	Ser	Pro										
																	35								
																	40								
																	45								
gac ccc tac gcc aag cag ata gac ggt ttg gcc aac gcc agt tcg tcc 192																									
Asp	Pro	Tyr	Gly	Lys	Gln	Ile	Asp	Gly	Leu	Gly	Asn	Ala	Ser	Ser	Ser										
																	50								
																	55								
																	60								
acc agc aaa gcc gtg att ttg gac aag tcc gaa cgc acc gat cac gat 240																									
Thr	Ser	Lys	Ala	Val	Ile	Leu	Asp	Lys	Ser	Gln	Arg	Thr	Asp	His	Asp										
																	65								
																	70								
																	75								
																	80								
gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288																									
Val	Asp	Tyr	Leu	Phe	Gly	Gln	Val	Ser	Ile	Asp	Lys	Pro	Phe	Val	Asp										
																	85								
																	90								
																	95								
tgg agt gcc aac tgc gcc aac ctg acc gcc gcc gtg gcc gca ttt gcc 336																									
Trp	Ser	Gly	Asn	Cys	Gly	Asn	Leu	Thr	Ala	Ala	Val	Gly	Ala	Phe	Ala										
																	100								
																	105								
																	110								
ile gag caa gcc tgc gtc gat aaa tcc aaa atc cct tca gac gcc ccg 384																									
Ile	Glu	Gln	Gly	Leu	Val	Asp	Lys	Ser	Lys	Ile	Pro	Ser	Asp	Gly	Pro										
																	115								
																	120								
																	125								
tgt acc gct aca atc tgg cag aaa aac atc gcc aaa acc att att gcc 432																									
Cys	Thr	Val	Lys	Ile	Trp	Gln	Lys	Asn	Ile	Gly	Lys	Thr	Ile	Ile	Ala										
																	130								
																	135								
																	140								
cat gta ccg atg caa aac gcc gca gtt ttg gaa acg gcc gat ttt gag 480																									

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
145 150 155 160

ctc gac ggc gta acg ttc ccg gca gcc gaa gta caa atc gaa ttt ctt 528
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
165 170 175

gat cca gcc gac ggc gaa ggc agt atg ttc cca acc ggc aat ttg gtc 576
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val
180 185 190

gat gaa att gat gtg ccg aat ata ggc cgt ttg aaa gcc acg ctc atc 624
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile
195 200 205

aac gcg ggc att ccg acc gtt ttc ctg aat gcc gcc gac ttg ggc tac 672
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr
210 215 220

acg ggc aaa gag ttg caa gac gac atc aac aac gat gcc gca gct ttg 720
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu
225 230 235 240

gaa aaa ttc gag aaa atc cgc gct tac ggt gcg ctg aaa atg ggt cta 768
Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
245 250 255

atc agc gac gta tcc gaa gct gcc gcc cgc gcg cac acg ccg aaa gtc 816
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
260 265 270

gcc ttc gtc gcg ccc gcc gcc gat tac acc gcc tcc agt ggc aaa acc 864
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
275 280 285

gtg aat gcc gcc gac atc gat ttg ctg gta cgc gcc ctg agc atg ggc 912
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
290 295 300

aaa ttg cac cac gcg atg atg ggt acc gcc tct gtt gcc att gcg acc 960
Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
305 310 315 320

gcc gcc gcc gtg ccc ggt acg ctg gtc aac ctt gcc gca ggg gcg gga 1008
Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly
325 330 335

acg cgt aaa gaa gtg cgc ttc ggg cat cct tcc gcc aca ttg cgc gtc 1056
Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
340 345 350

ggt gca gcc gcc gaa tgt cag gac gga caa tgg acg gcc acc aaa gcg 1104
Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
355 360 365

gtt atg agc cgc agc gca cgc gtg atg atg gaa ggt tgg gtc agg gtg 1152
Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
370 375 380

ccg gaa gat tgt ttt taa 1170
Pro Glu Asp Cys Phe
385

<210> 44

<211> 389

<212> PRT

<213> Neisseria meningitidis

<400> 44

Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser
1 5 10 15

Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
20 25 30

Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
35 40 45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 55 60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
65 70 75 80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
85 90 95

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110

Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro
115 120 125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
130 135 140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
145 150 155 160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
165 170 175

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val
180 185 190

Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile
195 200 205

Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr
210 215 220

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu
225 230 235 240

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
245 250 255

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
260 265 270

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<210> 45
<211> 954
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(951)
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[illegible]

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100 105 110	
cgc atc ggc cag cag gat aat cgg ttt gcc gcc ggg cgg cac ctg cac Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His	384
115 120 125	
ggt tcc tgc ctg aac agc gtg gga cag cat ttc caa agg ttg cga cag Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln	432
130 135 140	
ggt cag cgg ctg tcc gtc gaa ggc gta gcc cat gcg gct gct atc gct Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala	480
145 150 155 160	
ttg cag cgt cca cgt ttc cgg ttc cag att cag acg ccc ttt ttc act Leu Gln Arg Pro Arg Phe Pro Phe Gln Thr Pro Phe Phe Thr	528
165 170 175	
gaa agc ggc ata ttc cga cga agg aac aag gtg gat ggt atc ggt aaa Gly Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys	576
180 185 190	
cgg tat cgg ggc aat gcc gac ttt gga caa ttc ctg cgc acc ttt gcc Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Trp Phe Ala	624
195 200 205	
gat ggg gag ata atc gcc ttt tgg cag cat tct gcc ctg atg gcc gcc Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala	672
210 215 220	
gaa atc ggc ttt cag gtc ggt gtc tct cga acc cat cac ttc cgg cac Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His	720
225 230 235 240	
atc aaa tcc gcc cgc cac gca cac ata gcc gta cat gcc ctg cac ggc Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly	768
245 250 255	
acg cac cat ttt caa ggt ctg ccc ttt cgg ggc ggt ata acg cca ata Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile	816
260 265 270	
cga ata gac cgg ttc gcc gtc caa ttc cgc ctg ata cac ggc acc ggt Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly	864
275 280 285	
gag aca aaa cgg cgt atc cgg ttc aaa cac cag cat tat ccc gcc caa Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln	912
290 295 300	
agc gat ttc gat tgc ggc cgt gcc ttc gtc gct gcc caa taa Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln	954
305 310 315	

<210> 46
<211> 317
<212> PRT
<213> Neisseria meningitidis

<400> 46
Met Arg Thr Pro Phe Cys Trp Ala Tyr Ala Asn Ala Ala Arg Ile Ser
1 5 10 15
Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile
20 25 30
Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala
35 40 45
Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile
50 55 60
Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr
65 70 75 80
Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
85 90 95
Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu
100 105 110
Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His
115 120 125
Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln
130 135 140
Gly Gln Arg Leu Ser Val Gln Ala Val Ala His Ala Val Ala Ile Ala
145 150 155 160
Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr
165 170 175
Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys
180 185 190
Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala
195 200 205
Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala
210 215 220
Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His
225 230 235 240
Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly
245 250 255
Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile
260 265 270
Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly
275 280 285
Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln
290 295 300
Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln
305 310 315

ggc ggc tgg cag att atc ggc aga acc gaa tta ccc ttg ttc cga gcc 576
Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
180 185 190

gat ttg aat ccg ccg acc ctg ctg gcg gcg ggt gac caa gtc cgc ttt 624
Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
195 200 205

gtt gca gaa agg att gag cca tga 648
Val Ala Glu Arg Ile Glu Pro
210 215

<210> 48

<211> 215

<212> PRT

<213> *Neisseria meningitidis*

<400> 48

Met Arg Ile Glu Ile Thr Pro Ile Ser Glu Ser Ala Leu Val Cys Arg
1 5 10 15

Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe
20 25 30

Ala Ala Ala Leu Gly Gln His Asp Arg Ile Glu Glu Val Val Val Gly
35 40 45

Met Asn Asn Leu Thr Val Thr Arg Phe Asp Thr Asp Leu Ala Thr
50 55 60

Leu Ala Asp Glu Leu Glu Tyr Val Tyr Glu His Thr Ala Val Thr Asp
65 70 75 80

His Gln Gly Lys Leu Val Gln Ile Pro Val Cys Tyr Gly Gly Glu Tyr
85 90 95

Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser
100 105 110

Glu Ile Val Arg Arg His Thr Ala Cln Thr Tyr Thr Val Gln Met Met
 115 120 125

Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu
130 135 140

His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser
145 150 155 160

Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro
165 170 175

Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
180 185 190

Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
195 200 205

Val	Ala	Glu	Arg	Ile	Glu	Pro
210						215

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<210> 49
 <211> 930
 <212> DNA
 <213> *Neisseria meningitidis*

<220>
 <221> CDS
 <222> (1)..(927)

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atg att cac gtt tgc gca gtc cag gca cgg gcg cat att cag gat acc 48
Met Ile His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asp Thr
      1             5             10             15

gga cgc tac gga cac cgg cgt tac ggc atc ggt cat gcc ggt gcg atg 96
Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
      20             25             30

gac acg gtt gct ttg gcg gcg ggt aat att tta ttg ggc aac gac gaa 144
Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu
      35             40             45

ggc acg gcc gca atc gaa atc gct ttg ggc ggg ata atg ctg gtc ttt 192
Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
      50             55             60

gaa cgs gat acg ccg ttt tgt ctc acc ggt gcc gtc tat cag gcg gaa 240
Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
      65             70             75             80

ttg gac ggc gaa cgg gtc tat tgc tat tgg cgt tat acc gcc cgc aaa 288
Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
      85             90             95

ggg cag acc ttg aaa atg gtc cgt gcc gtc cag ggc atg tac ggc tat 336
Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr
      100            105            110

gtg tgc gtc gcg ggc gga ttt gat gtc cgg gaa gtc atg ggt tgc aga 384
Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg
      115            120            125

agc acc gac ctg aaa gcc ggt ttc ggc ggc cat cag gcc aga atg ctg 432
Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu
      130            135            140

caa aaa ggc gat tat ctc ccc atc ggc aaa ggt gcg cag gaa ttg tcc 480
Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser
      145            150            155            160

aaa gtc ggc att gcc cgg ata cgg ttt acc gat acc atc cac ctt gtt 528
Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val
      165            170            175

cct tgc tgc gaa tat gcc gct ttc agt gaa aaa ggc cgt ctg aat ctg 576
Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu
      180            185            190
    
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<210> 50
<211> 309
<212> PRT
<213> Neisseria meningitidis
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Met Ile His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asp Thr
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Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
  20          25          30
Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu
  35          40          45
Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
  50          55          60
Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
  65          70          75          80
Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
  85          90          95
Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr
  100          105          110

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Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg
115 120 125

Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu
130 135 140

Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser
145 150 155 160

Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val
165 170 175

Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu
180 185 190

Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr
195 200 205

Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu
210 215 220

Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys
225 230 235 240

Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys
245 250 255

Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg
260 265 270

Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr
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Ala Leu Arg Arg Lys Asn Gln Val Tyr Leu Asn Gln Ile Arg Arg Ile
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Thr His Glu Ala Gly
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ttc gcc tct gga ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
20 25 30

ttt	tta	ttc	agt	cac	ata	ggc	ttc	gat	ttg	agt	tgc	att	act	gtc	att	144
Leu	Leu	Phe	Ser	His	Ile	Gly	Ile	Asp	Leu	Ser	Ser	Ile	Thr	Val	Ile	
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att	tct	gta	ttt	atg	gtc	ggc	ttg	ggc	gta	ggc	gcg	tat	tcc	ggc	gga	192
Ile	Ser	Val	Phe	Met	Val	Gly	Leu	Gly	Val	Gly	Ala	Tyr	Phe	Gly	Gly	
		50				55					60					
cgc	att	gct	gac	cgt	ttt	cct	tca	agt	atc	atc	ccc	ctg	ttt	tgc	atc	240
Arg	Ile	Ala	Asp	Arg	Phe	Pro	Ser	Ser	Ile	Ile	Pro	Leu	Phe	Cys	Ile	
		65			70						75				80	
gct	gaa	gta	tcc	atc	ggc	ctg	ttc	ggc	ttg	gta	agc	agg	ggc	ctg	att	288
Ala	Glu	Val	Ser	Ile	Gly	Leu	Phe	Gly	Leu	Val	Ser	Arg	Gly	Leu	Ile	
				85					90					95		
tcc	ggc	ttg	ggg	cat	ctt	tta	gtc	gag	gct	gat	ttg	ccc	atc	atc	gct	336
Ser	Gly	Leu	Gly	His	Leu	Leu	Val	Glu	Ala	Asp	Leu	Pro	Ile	Ile	Ala	
			100					105					110			
gct	gcc	aat	ttc	ctc	tta	ttg	ctg	ccc	cct	acc	ttt	atg	atg	ggc	gcg	384
Ala	Ala	Asn	Phe	Leu	Leu	Leu	Leu	Pro	Thr	Phe	Met	Met	Met	Gly	Ala	
		115					120				125					
acc	ttg	ccc	ttg	ctg	acc	tgt	ttt	ttt	aac	cgg	aaa	ata	cat	aat	gtt	432
Thr	Leu	Pro	Leu	Leu	Thr	Cys	Phe	Phe	Asn	Arg	Lys	Ile	His	Asn	Val	
		130				135					140					
ggc	gag	tct	atc	ggc	acc	tta	tat	ttt	ttc	aac	act	ttg	ggc	gcg	gca	480
Gly	Glu	Ser	Ile	Gly	Thr	Leu	Tyr	Phe	Phe	Asn	Thr	Leu	Gly	Ala	Ala	
	145			150					155					160		
ccc	gga	cgc	ctt	gcc	gcc	gcc	gaa	ttt	ttr	tac	gtc	ttt	ttt	acc	ctc	528
Leu	Gly	Ser	Leu	Ala	Ala	Ala	Glu	Phe	Phe	Tyr	Val	Phe	Phe	Thr	Leu	
			165					170					175			
tcc	caa	acc	att	ggc	ctg	aca	gct	tgc	ttt	aac	ctt	ccg	att	gct	gct	576
Ser	Gln	Thr		Ile	Ala	Leu	Thr	Ala	Cys	Phe	Asn	Leu	Ile	Ile	Ala	
		180						185				190				
tca	gta	tgc	tgc	gtt	aca	gaa	agg	atg	gat	ata	gtg	aac	act	aaa	ccg	624
Ser	Val	Cys	Cys	Val	Thr	Glu	Arg	Met	Asp	Ile	Val	Asn	Thr	Lys	Pro	
		195					200				205					
aat	act	agt	ttg	att	tat	atg	ctt	tct	ttc	ctt	agc	ggc	tta	ttg	agc	672
Asn	Thr	Ser	Leu	Ile	Tyr	Met	Leu	Ser	Phe	Leu	Ser	Gly	Leu	Leu	Ser	
		210				215					220					
ttg	ggc	ata	gaa	gtc	ttg	tgg	gta	agg	atg	ttt	tcg	ttc	gca	gca	cag	720
Leu	Gly	Ile	Glu	Val	Leu	Tyr	Val	Arg	Met	Phe	Ser	Phe	Ile	Ala	Gln	
	225			230						235			240			

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Val	Asp	Pro	Pro	Pro	Ile	Gly	Gln	Cys	Phe	Leu	Trp	Ala	Gly	Ile	Ala	
	275						280					285				
gac	ttt	ttg	att	ttg	ggg	gct	ggc	tgg	ttg	ttg	acg	ggg	ttt	ccc	ggc	912
Asp	Phe	Leu	Ile	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Thr	Gly	Phe	Ser	Gly	
	290					295					300					
ttc	gtc	cac	cac	ggc	ggg	atc	ttc	att	acc	ctg	tct	ggc	gtc	gtc	aga	960
Phe	Val	His	His	Ala	Gly	Ile	Phe	Ile	Thr	Leu	Ser	Ala	Val	Val	Arg	
	305				310					315					320	
ggg	ttg	att	ttc	ccg	ctc	gta	cac	cat	gtg	ggg	acg	gat	ggc	aac	aaa	1008
Gly	Leu	Ile	Phe	Pro	Leu	Val	His	His	Val	Gly	Thr	Asp	Gly	Asn	Lys	
				325					330					335		
ccc	gga	cga	cag	ggt	ttc	aat	ggt	tat	ttc	gcc	aac	ggt	gcc	ggc	agt	1056
Ser	Gly	Arg	Gln	Val	Ser	Asn	Val	Tyr	Phe	Ala	Asn	Val	Ala	Gly	Ser	
			340					345					350			
gca	ttg	ggg	ccg	gtc	ctt	atc	ggc	ttt	gtg	ata	ctt	gat	ttc	ttg	ccc	1104
Ala	Leu	Gly	Pro	Val	Leu	Ile	Gly	Phe	Val	Ile	Leu	Asp	Phe	Leu	Ser	
			355				360					365				
acc	caa	cag	att	tac	ctg	ctc	atc	tgt	ctg	att	ttc	ggt	ggt	gtc	ccc	1152
Thr	Gln	Gln	Ile	Tyr	Leu	Leu	Ile	Cys	Leu	Ile	Ser	Ala	Ala	Val	Pro	
	370					375					380					
ttg	ttt	tgt	aca	ctg	ttc	caa	aaa	agt	ctc	cga	ctg	aat	gca	gtg	tcg	1200
Leu	Phe	Cys	Thr	Leu	Phe	Gln	Lys	Tyr	Leu	Arg	Leu	Asn	Ala	Val	Ser	
	385				390					395					400	
gtc	gca	ggt	ccc	cta	atg	ttc	ggt	atc	ctc	atg	ttc	ctc	ctg	ccg	gat	1248
Val	Ala	Val	Ser	Leu	Met	Phe	Gly	Ile	Leu	Met	Phe	Leu	Leu	Phe	Asp	
			405					410					415			
ttc	gtc	ttt	caa	aac	atc	gct	gac	agc	ccg	gac	ccg	ctg	att	gaa	aac	1296
Ser	Val	Phe	Gln	Asn	Ile	Ala	Asp	Cys	Pro	Asp	Arg	Leu	Ile	Glu	Asn	
			420				425					430				
aaa	cac	ggc	ctc	ggt	ggg	gct	tac	cat	aga	gat	ggg	gat	aag	gtc	gtt	1344
Lys	His	Gly	Ile	Val	Glu	Ala	Val	Tyr	His	Arg	Asp	Gly	Asp	Lys	Val	
			435				440					445				
tat	ggg	ggc	aat	gta	tac	gac	ggc	gca	tac	aat	acc	gat	gta	ttc	aac	1392
Tyr	Gly	Ala	Asn	Val	Tyr	Asp	Gly	Ala	Tyr	Asn	Thr	Asp	Val	Phe	Asn	
	450					455					460					
agt	gtc	aac	ggc	atc	gaa	agg	ggc	tat	ctg	cta	ccc	ttc	ctg	aag	ctt	1440
Ser	Val	Asn	Gly	Ile	Glu	Arg	Ala	Tyr	Leu	Leu	Pro	Ser	Leu	Lys	Ser	
	465				470											

atc aat cgc gca tac cgt agc ctt atc gcg gac gag cgc caa atc gcc 1584
 Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala
 515 520 525

cgc ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt ags 1632
 Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
 530 535 540

aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg 1680
 Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
 545 550 555 560

aat acg act tgg tac tgg cgt gcc tat tcc acc aac ctg ttg agt gcg 1728
 Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
 565 570 575

gaa ttt tta aaa cag ggg caa agc cac ctt acc cgc gat ggt att gta 1776
 Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
 580 585 590

atg ttt aat acc acg cac agc cgc cat ttt gct acc gcc gta cac 1824
 Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
 595 600 605

agt att ctc tat gca tac tgc tat ggg cat atg gta gtc ggc tgc gca 1872
 Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
 610 615 620

acc cgc gta gtt ttc cct aat aaa gaa ctg ttc aag caa cgt ctc tcc 1920
 Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
 625 630 635 640

cgc ttg att tgg cgc gaa agc ggt ags cao gta ttt gac agc agc acc 1952
 Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
 645 650 655

gtg gat gct goa gta taa aag gtt gtc tcc cgt arg ctg att gag atg 2016
 Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met
 660 665 670

acg gaa cct tgc gct ggg cgc gaa gtc att acc gac gat aat atg att 2064
 Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile
 675 680 685

gta gaa tac aaa tac ggc aga ggg att taa 2094
 Val Glu Tyr Lys Tyr Gly Arg Gly Ile
 690 695

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 <213> Neisseria meningitidis

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Ile	Ser	Val	Phe	Met	Val	Gly	Leu	Gly	Val	Gly	Ala	Tyr	Phe	Gly	Gly
50						55						60			
Arg	Ile	Ala	Asp	Arg	Phe	Pro	Ser	Ser	Ile	Ile	Pro	Leu	Phe	Cys	Ile
65						70						75			
Ala	Glu	Val	Ser	Ile	Gly	Leu	Phe	Gly	Leu	Val	Ser	Arg	Gly	Leu	Ile
			85						90						
Ser	Gly	Leu	Gly	His	Leu	Leu	Val	Glu	Ala	Asp	Leu	Pro	Ile	Ile	Ala
			100						105						
Ala	Ala	Asn	Phe	Leu	Leu	Leu	Leu	Leu	Pro	Thr	Phe	Met	Met	Gly	Ala
115						120						125			
Thr	Leu	Pro	Leu	Leu	Thr	Cys	Phe	Phe	Asn	Arg	Lys	Ile	His	Asn	Val
130						135						140			
Gly	Glu	Ser	Ile	Gly	Thr	Leu	Tyr	Phe	Phe	Asn	Thr	Leu	Gly	Ala	Ala
145						150						155			
Leu	Gly	Ser	Leu	Ala	Ala	Glu	Phe	Phe	Tyr	Val	Phe	Phe	Thr	Leu	
			165						170						
Ser	Gln	Thr	Ile	Ala	Leu	Thr	Ala	Cys	Phe	Asn	Leu	Leu	Ile	Ala	Ala
			180						185						
Ser	Val	Cys	Cys	Val	Thr	Glu	Arg	Met	Asp	Ile	Val	Asn	Thr	Lys	Pro
195						200						205			
Asn	Thr	Ser	Leu	Ile	Tyr	Met	Leu	Ser	Phe	Leu	Ser	Gly	Leu	Leu	Ser
210						215						220			
Leu	Gly	Ile	Glu	Val	Leu	Trp	Val	Arg	Met	Phe	Ser	Phe	Ala	Ala	Gln
225						230						235			
Ser	Val	Pro	Gln	Ala	Phe	Ser	Phe	Thr	Leu	Ala	Tyr	Phe	Leu	Thr	Gly
			245						250						
Ile	Ala	Val	Gly	Ala	Tyr	Phe	Gly	Lys	Arg	Ile	Cys	Arg	Ser	Arg	Phe
260									265						
Val	Asp	Ile	Pro	Phe	Ile	Gly	Gln	Cys	Phe	Leu	Trp	Ala	Gly	Ile	Ala
275						280						285			
Asp	Phe	Leu	Ile	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Thr	Gly	Phe	Ser	Gly
290						295						300			
Phe	Val	His	His	Ala	Gly	Ile	Phe	Ile	Thr	Leu	Ser	Ala	Val	Val	Arg
305						310						315			
Gly	Leu	Ile	Phe	Pro	Leu	Val	His	His	Val	Gly	Thr	Asp	Gly	Asn	Lys
			325						330						
Ser	Gly	Arg	Gln	Val	Ser	Asn	Val	Tyr	Phe	Ala	Asn	Val	Ala	Gly	Ser
340						345						350			

Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser
355 360 365

Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro
370 375 380

Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser
385 390 395 400

Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp
405 410 415

Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn
420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val
435 440 445

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn
450 455 460

Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser
465 470 475 480

Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala
485 490 495

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu
500 505 510

Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala
515 520 525

Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
530 535 540

Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
545 550 555 560

Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
595 600 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
610 615 620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
645 650 655

Val Asp Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met
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Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile
675 680 685

Val Glu Tyr Lys Tyr Gly Arg Gly Ile
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<212> PRT

<213> Neisseria meningitidis

<400> 53

Cys Leu Gly Gly Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly
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Gly Thr Gly Ile Gly Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala
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Ala Val Ser Tyr Ala Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser
35 40 45

Met Leu Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala
50 55 60

Lys Ile Asn Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn
65 70 75 80

Pro Asn Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu
85 90 95

Ala Gly Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly
100 105 110

Glu Ser Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu
115 120 125

His Gly Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys
130 135 140

Glu Ala Pro Glu Asp Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp
145 150 155 160

Asp Glu Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His
165 170 175

Val Lys Glu Ile Gly His Ile Asp Val Val Ser His Ile Ile Gly Gly
180 185 190

Arg Ser Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr
195 200 205

Leu His Ile Met Asn Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser
210 215 220

Ala Ala Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg
225 230 235 240

Ile	Val	Asn	Asn	Ser	Phe	Gly	Thr	Thr	Ser	Arg	Ala	Gly	Thr	Ala	Asp
				245					250					255	
His	Phe	Gln	Ile	Ala	Asn	Ser	Glu	Glu	Gln	Tyr	Arg	Gln	Ala	Leu	Leu
			260					265					270		
Ala	Tyr	Ser	Gly	Gly	Asp	Lys	Thr	Asp	Glu	Gly	Ile	Arg	Leu	Met	Gln
			275				280					285			
Gln	Ser	Asp	Tyr	Gly	Asn	Leu	Ser	Tyr	His	Ile	Arg	Asn	Lys	Asn	Met
			290			295					300				
Leu	Phe	Ile	Phe	Ser	Ala	Ser	Asn	Asp	Ala	Gln	Ala	Gln	Pro	Asn	Thr
305					310					315					320
Leu	Thr	Leu	Leu	Pro	Phe	Tyr	Glu	Lys	Asp	Ala	Gln	Lys	Gly	Ile	Ile
				325					330					335	
Thr	Val	Ala	Gly	Val	Asp	Arg	Ser	Gly	Glu	Lys	Phe	Asn	Gly	Ser	Asn
			340					345					350		
His	Cys	Gly	Ile	Thr	Ala	Met	Trp	Cys	Leu	Ser	Ala	Pro	Tyr	Glu	Ala
			355				360					365			
Ser	Val	Arg	Phe	Thr	Arg	Thr	Asn	Pro	Ile	Gln	Ile	Ala	Gly	Thr	Ser
			370			375						380			
Phe	Ser	Ala	Pro	Ile	Val	Thr	Gly	Thr	Ala	Ala	Leu	Leu	Leu	Gln	Lys
395					390					395					400
Tyr	Pro	Trp	Met	Ser	Asn	Asp	Asn	Leu	Arg	Thr	Thr	Leu	Leu	Thr	Thr
				405					410					415	
Ala	Gln	Asp	Ile	Gly	Ala	Val	Gly	Val	Asp	Ser	Lys	Phe	Gly	Trp	Gly
			420					425					430		
Leu	Leu	Asp	Ala	Gly	Lys	Ala	Met	Asn	Gly	Pro	Ala	Ser	Phe	Pro	Phe
			435				440					445			
Gly	Asp	Phe	Thr	Ala	Asp	Thr	Lys	Gly	Thr	Ser	Asp	Ile	Ala	Tyr	Ser
			450			455					460				
Phe	Arg	Asn	Asp	Ile	Ser	Gly	Thr	Gly	Gly	Leu	Ile	Lys	Lys	Gly	Gly
			465		470				475					480	
Ser	Gln	Leu	Gln	Leu	His	Gly	Asn	Asn	Thr	Tyr	Thr	Gly	Lys	Thr	Ile
			485						490					495	
Ile	Glu	Gly	Gly	Ser	Leu	Val	Leu	Tyr	Gly	Asn	Asn	Lys	Ser	Asp	Met
			500					505					510		
Arg	Val	Glu	Thr	Lys	Gly	Ala	Leu	Ile	Tyr	Asn	Gly	Ala	Ala	Ser	Gly
			515				520					525			
Gly	Ser	Leu	Asn	Ser	Asp	Gly	Ile	Val	Tyr	Leu	Ala	Asp	Thr	Asp	Arg
			530			535						540			
Ser	Gly	Ala	Asn	Glu	Thr	Val	His	Ile	Lys	Gly	Asp	Leu	Gln	Leu	Gly
545					550					555					560

Gly	Glu	Gly	Thr	Leu	Tyr	Thr	Arg	Leu	Gly	Lys	Leu	Leu	Lys	Val	Asp	575
																565
Gly	Thr	Ala	Met	Thr	Gly	Gly	Lys	Leu	Tyr	Met	Ser	Ala	Arg	Gly	Lys	
																580
Gly	Ala	Gly	Tyr	Leu	Asn	Arg	Thr	Gly	Gln	Arg	Val	Pro	Phe	Leu	Ser	
																595
Ala	Ala	Lys	Ile	Gly	Arg	Asp	Tyr	Ser	Phe	Phe	Thr	Asn	Ile	Glu	Thr	
																610
Asp	Gly	Gly	Leu	Leu	Ala	Ser	Leu	Asp	Ser	Val	Glu	Lys	Thr	Ala	Gly	
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Ser	Glu	Gly	Asp	Thr	Leu	Ser	Tyr	Tyr	Val	Arg	Arg	Gly	Asn	Ala	Ala	
																645
Arg	Thr	Ala	Ser	Ala	Ala	Ala	His	Ser	Ala	Pro	Ala	Gly	Leu	Lys	His	
																660
Ala	Val	Glu	Gln	Gly	Gly	Ser	Asn	Leu	Glu	Asn	Leu	Met	Val	Glu	Leu	
																675
Asp	Ala	Ser	Glu	Ser	Ser	Ala	Thr	Pro	Glu	Thr	Val	Glu	Thr	Ala	Ala	
																690
Ala	Asp	Arg	Thr	Asp	Met	Pro	Gly	Ile	Arg	Pro	Tyr	Gly	Ala	Thr	Phe	
																705
Arg	Ala	Ala	Ala	Ala	Val	Gln	His	Ala	Asn	Ala	Ala	Asp	Gly	Val	Arg	
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Ile	Phe	Asn	Ser	Leu	Ala	Ala	Thr	Val	Tyr	Ala	Asp	Ser	Thr	Ala	Ala	
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His	Ala	Asp	Met	Gln	Gly	Arg	Arg	Leu	Lys	Ala	Val	Ser	Asp	Gly	Leu	
																755
Asp	His	Asn	Ala	Thr	Gly	Leu	Arg	Val	Ile	Ala	Gln	Thr	Gln	Gln	Asp	
																770
Gly	Gly	Thr	Trp	Glu	Gln	Gly	Gly	Val	Glu	Gly	Lys	Met	Arg	Gly	Ser	
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Thr	Gln	Thr	Val	Gly	Ile	Ala	Ala	Lys	Thr	Gly	Glu	Asn	Thr	Thr	Ala	
																805
Ala	Ala	Thr	Leu	Gly	Met	Gly	His	Ser	Thr	Trp	Ser	Glu	Asn	Ser	Ala	
																820
Asn	Ala	Lys	Thr	Asp	Ser	Ile	Ser	Leu	Phe	Ala	Gly	Ile	Arg	His	Asp	
																835
Ala	Gly	Asp	Ile	Gly	Tyr	Leu	Lys	Gly	Leu	Phe	Ser	Tyr	Gly	Arg	Tyr	
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Lys	Asn	Ser	Ile	Ser	Arg	Ser	Thr	Gly	Ala	Asp	Glu	His	Ala	Glu	Gly	
																865

Ser Val Asn Gly Thr Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn
885 890 895

Val Pro Phe Ala Ala Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg
900 905 910

Tyr Asp Leu Leu Lys Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu
915 920 925

Gly Trp Ser Gly Asn Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala
930 935 940

Gly Leu Lys Leu Ser Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala
945 950 955 960

Thr Ala Gly Val Glu Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr
965 970 975

Gly Gly Phe Thr Gly Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg
980 985 990

Asn Met Pro His Thr Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu
995 1000 1005

Phe Gly Asn Gly Trp Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser
1010 1015 1020

Lys Gln Tyr Gly Asn His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
1025 1030 1035 1040

<210> 54
<211> 858
<212> DNA
<213> Neisseria gonorrhoeae

<220>
<221> CDS
<222> (1)..(855)

<400> 54
atg tct gaa gaa aaa ttg aaa atg agt ttc gag cca acc gta atc gaa 48
Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu
1 5 10 15

cat ttg ggt gta aag atg tat tgc cac act gtt cct gcg att gcc gag 96
His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu
20 25 30

ttg ata gcg aat gcc tac gat gca tgt gct acg gaa gtg gaa gtt agg 144
Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
35 40 45

tta ttc gat aaa cgg gag cat aaa atc gtt att aaa gat aat ggc ata 192
Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
50 55 60


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gga atg agc ttc gat gaa atc aat gat ttt tat ttg aga atc ggt cgg 240
Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg
65 70 75 80

aac aga agg gaa gaa aaa caa gcc tcc ccg tgc gga aga att cca acg 288
Asn Arg Arg Glu Gln Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr
85 90 95

ggg aaa aaa ggt ctt ggt aaa ttg gca tta ttc agg ctt ggc aac aaa 336
Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys
100 105 110

atc gaa atc tct act atc caa gga aac gaa cgg gtt act ttt acc ttg 384
Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu
115 120 125

gat tat gca gag att aaa aaa agt gag cgt att tat caa ccg gag ttt 432
Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe
130 135 140

cag aaa gag tct gtt aaa ccc aat acc gaa aac gga aca act ata act 480
Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr
145 150 155 160

tta acc gag ctg acg aaa aaa caa gga tac ccg tta gat aat tat gtg 528
Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val
165 170 175

ggg cat ctt tcc cgt tta ttt gat ttt ccg gct cag gat ttt aaa atc 576
Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile
180 185 190

aaa gta agc ttg aac ggc tgc gaa cca aga atc att gac gga aac cta 624
Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu
195 200 205

aaa tat aat ctt gtt acc cca caa ttc gaa tgg gaa tac cag gat cta 672
Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
210 215 220

gca acc aat att tca tgc tta tct tca aaa ttc gaa cag tat gaa tac 720
Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
225 230 235 240

agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag 768
Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys
245 250 255

aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat 816
Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn
260 265 270

atg ccc gag ttt ttc act gat agc gaa tcc agc cat ttc taa 858
Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe
275 280 285

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<210> 55
 <211> 285
 <212> PRT
 <213> Neisseria gonorrhoeae

<400> 55
Met Ser Glu Glu Lys Leu Lys Met Ser Phe Glu Pro Thr Val Ile Glu
1 5 10 15
His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu
20 25 30
Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
35 40 45
Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
50 55 60
Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg
65 70 75 80
Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr
85 90 95
Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys
100 105 110
Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu
115 120 125
Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe
130 135 140
Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr
145 150 155 160
Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val
165 170 175
Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile
180 185 190
Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu
195 200 205
Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
210 215 220
Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
225 230 235 240
Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys
245 250 255
Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn
260 265 270
Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe
275 280 285

<210> 56
<211> 1575
<212> DNA
<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(1572)

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<400> 56
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Met Lys Lys Ser Leu Phe Val Leu Phe Leu Tyr Ser Ser Leu Leu Thr
      1              5              10              15

gcc agc gaa atc gcc tat cgc ttt gta ttc gga att gaa acc tta cgg 96
Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro
      20              25              30

gct gca aaa atg gcg gaa acg ttt gcg ctg aca ttt atg att gct gcg 144
Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala
      35              40              45

ctg tat ctg ttt gcg cgt tat aag gct tgg cgg ctg ctg att gcg gtg 192
Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val
      50              55              60

ttt ttc gcg ttc agc atg att gcc aac aat gtg cat tac gcg gtt tat 240
Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr
      65              70              75              80

caa agc tgg atg acg ggt att aac tat tgg ctg atg ctg aaa gag gtt 288
Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val
      85              90              95

acc gaa gtc gcc agc gcg gcc gcg tgg atg ttg gat aag ttg tgg ctg 336
Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu
      100             105             110

cct gct ttg tgg gcc gtg gcg gaa gtc atg ttg ttt tgc agc ctt gcc 384
Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala
      115             120             125

aag ttc cgc cgt aag acg cat ttt tct gcc gat ata ctg ttt gcc ttc 432
Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe
      130             135             140

cta atg ctg atg att ttc gtg cgt tgg ttc gac acg aaa caa gag cac 480
Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His
      145             150             155             160

ggt att tgg ccc aaa ccg aca tac agc cgc atc aaa gcc aat tat ttc 528
Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe
      165             170             175

agc ttc ggt tat ttt gtc ggg cgc gtg ttg ccg tat cag ttg ttt gat 576
Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp
      180             185             190

tta agc aag atc cct gtg ttc aaa cag cct gct cca agc aaa atc ggg 624
Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly

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195	200	205	
caa ggc agt att caa aat atc gtc ctg att atg ggc gaa agc gaa agc Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser 210 215 220			672
gcg gcg cat ttg aaa ttg ttt ggt tac ggg cgc gaa act tcg ccg ttt Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe 225 230 235 240			720
tta acc cgg ctg tcg caa gcc gat ttt aag ccg att gtg aaa caa agt Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser 245 250 255			768
tat tcc gca ggc ttt atg acg gca gta tcc ctg ccc agt ttc ttt aac Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn 260 265 270			816
gtc ata ccg cac gcc aac ggc ttg gaa caa atc agc ggc ggc gat acc Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr 275 280 285			864
aac atg ttc cgc ctg gcc aaa gag cag ggc tat gaa acg tat ttt tac Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr 290 295 300			912
agt gcc cag gct gaa aac caa atg gca att ttg aac tta atc ggt aag Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys 305 310 315 320			960
aaa tgg ata gac cat ctg att cag ccg acg caa ctt ggc tac ggc aac Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn 325 330 335			1008
ggc gac aat atg ccc gat gag aag ctg ctg ccg ttg ttc gac aaa atc Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile 340 345 350			1056
aat ttg cag cag ggc agg cat ttt atc gtg ttg cac caa cgc ggt tcg Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser 355 360 365			1104
cac gcc cca tac ggc gca ttg ttg cag cct caa gat aaa gta ttc ggc His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly 370 375 380			1152
gaa gcc gat att gtg gat aag tac gac aac acc atc cac aaa acc gac Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp 385 390 395 400			1200
caa atg att caa acc gta ttc gag cag ctg caa aag cag cct gac ggc Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly 405 410 415			1248
aac tgg ctg ttt gcc tat acc tcc gat cat ggc cag tat gtg cgc caa Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln 420 425 430			1296
gat atc tac aat caa ggc acg gtg cag ccc gac agc tat att gtg cct Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro 435 440 445			1344

435		440		445	
ctg gtt ttg tac agc ccg gat aag gcc gtg caa cag gct gcc aac cag					1392
Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln					
450		455		460	
gct ttt gcg cct tgc gag att gcc ttc cat cag cag ctt tca acg ttc					1440
Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe					
465		470		475	480
ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa					1488
Leu Ile His Thr Thr Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu					
485			490	495	
ggc tcg gta acg ggc aac ctg att ccg gcc gat gca gcc agc ttg aac					1536
Gly Ser Val Thr Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn					
500			505	510	
att cgc aac gcc aag gcg gaa tat gct tat ccg caa taa					1575
Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln					
515		520			

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<210> 57
<211> 524
<212> PRT
<213> Neisseria gonorrhoeae
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Met Lys Lys Ser Leu Phe Val Leu Phe Leu Tyr Ser Ser Leu Leu Thr
 1          5          10          15
Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro
 20          25          30
Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala
 35          40          45
Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val
 50          55          60
Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr
 65          70          75          80
Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val
 85          90          95
Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu
100          105          110
Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala
115          120          125
Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe
130          135          140
Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His
145          150          155          160
Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe

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165	170	175
Ser Phe Gly Tyr Phe Val Gly Arg	Val Leu Pro Tyr Gln Leu Phe Asp	
180	185	190
Leu Ser Lys Ile Pro Val Phe Lys	Gln Pro Ala Pro Ser Lys Ile Gly	
195	200	205
Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser		
210	215	220
Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe		
225	230	235
Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser		
245	250	255
Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn		
260	265	270
Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr		
275	280	285
Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr		
290	295	300
Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys		
305	310	315
Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn		
325	330	335
Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile		
340	345	350
Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser		
355	360	365
His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly		
370	375	380
Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp		
385	390	395
Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly		
405	410	415
Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln		
420	425	430
Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro		
435	440	445
Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln		
450	455	460
Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe		
465	470	475
Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu		

485

490

495

Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn
500 505 510

Ile Arg Asn Gly Lys Ala Glu Tyr Val Tyr Pro Gln
515 520

<210> 58

<211> 1314

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(1311)

<400> 58

atg ctg acg ttt atc gga ttg ctg att atc ggg gtc atc gta tgg ctg 48
Met Leu Thr Phe Ile Gly Leu Leu Ile Ile Gly Val Ile Val Trp Leu
1 5 10 15

tgg ctg acg gaa aaa ggg tgg ccc atc atc gca tta atc ttg gtg cgg 96
Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
20 25 30

ctg att ggg gcg tgg ctg ggg ggg ttt gat gta tcc caa tta aaa gaa 144
Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
35 40 45

ttt tat tgg ggc ggc acg aaa tgg gtg acg cag att gtg att atg ttt 192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe
50 55 60

atg ttt tcc att tgg ttt ttt gga atc atg aac gat gtg ggg ctg ttc 240
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
65 70 75 80

cgt ctg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg 288
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
85 90 95

gca gta agt gtg ggg acg gtc ctg gtg tgg gtg gca cag tgg gac 336
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
100 105 110

ggg gcg ggc gcg acg acg ttt tta tgg gtc gtc ccc gcc ctt ttg cgg 384
Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro
115 120 125

ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg 432
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
130 135 140

act tcc agc gcg ggg cta atc aac ctt ttg cgg cgg ggc ggg cgg atc 480
Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile
145 150 155 160

ggg cgg gtt gca agc gtg ttg ggc gca gat gtg ggc gaa ttg tat aaa 528
Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
165 170 175

cct ttg ttg acg gtg caa att atc ggt gtg gtg ttt atc ett gtg ctg 576
Pro Leu Leu Thr Val Gln Ile Ile ggt Val Val Phe Ile Leu Val Leu
180 185 190

tcc ctg ttt ttg ggt gtg cgt gaa aaa agg cgg att gtc cgg gag ttg 624
Ser Leu Phe Leu Gly Val Arg Gln Lys Arg Arg Ile Val Arg Glu Leu
195 200 205

ggc gcg ttg ccc gcc gtg gcg gat ttg ata aag ccg gcg cct ttg tgg 672
Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser
210 215 220

gaa gaa gaa caa aaa ttg gcg cgt ccg aaa ctg ttt tgg tgg aat gtc 720
Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
225 230 235 240

ctg ctg ttt ttg gcg gcg atg agc ctg ctt ttt tgg ggc atc ttc ccg 768
Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
245 250 255

ccg ggt tat gca ttt atg ctg gct gca acg gcg gcg ttg ctt ttg aat 816
Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn
260 265 270

tac cgc agc ccg cag gaa cag atg gag cgg att tat gcc cac gcc ggc 864
Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
275 280 285

ggc gcg gtg atg atg gcg tcc att att ttg ggc gca ggt acg ttt ttg 912
Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
290 295 300

ggg att ttg aag ggc gcg ggg atg ttg gac gcg att tcc aaa gac ctt 960
Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu
305 310 315 320

gtg cat atc ctg ccg gac gcg ttg ctg cct tat ctg cat att gcc atc 1008
Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
325 330 335

ggg gtg ttg ggt att ccg ctt gag ttg gtt ttg agt acg gac gct tat 1056
Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
340 345 350

tat ttc gga ctg ttt ccg att gtg gaa cag att acc tgg cag gcg ggc 1104
Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
355 360 365

ggt gca ccc gaa gcg gca ggc tat gcg atg ttg atc gcc agt atc gtc 1152
Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
370 375 380

ggg att ttt gtt acg ccg ctt tgg ccg gct ttg tgg atg ggt ttg ggt 1200
gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
385 390 395 400

[illegible]

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<210> 59
<211> 437
<212> PRT
<213> Neisseria gonorrhoeae
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400> 59

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Leu	Leu	Thr	Glu	Lys	Val	Ser	Pro	Ile	Ile	Ala	Leu	Ile	Leu	Val	Pro
			20					25						30	
Leu	Ile	Gly	Ala	Leu	Leu	Ala	Gly	Phe	Asp	Val	Ser	Gln	Leu	Lys	Glu
		35					40					45			
Phe	Tyr	Ser	Gly	Gly	Thr	Lys	Ser	Val	Thr	Gln	Ile	Val	Ile	Met	Phe
	50					55					60				
Met	Phe	Ser	Ile	Leu	Phe	Phe	Gly	Ile	Met	Asn	Asp	Val	Gly	Leu	Phe
65					70					75					80
Arg	Pro	Met	Ile	Gly	Gly	Leu	Ile	Lys	Leu	Thr	Arg	Gly	Asn	Ile	Val
				85						90				95	
Ala	Val	Ser	Val	Gly	Thr	Val	Leu	Val	Ser	Val	Val	Ala	Gln	Leu	Asp
			100					105						110	
Gly	Ala	Gly	Ala	Thr	Thr	Phe	Leu	Ser	Val	Val	Pro	Ala	Leu	Leu	Pro
		115					120					125			
Leu	Tyr	Lys	Arg	Leu	His	Met	Asn	Pro	Tyr	Leu	Leu	Phe	Leu	Leu	Leu
	130					135						140			
Thr	Ser	Ser	Ala	Gly	Leu	Ile	Asn	Leu	Leu	Pro	Arg	Gly	Gly	Pro	Ile
145					150					155					160
Gly	Arg	Val	Ala	Ser	Val	Leu	Gly	Ala	Asp	Val	Gly	Glu	Leu	Tyr	Lys
			165						170					175	
Pro	Leu	Leu	Thr	Val	Gln	Ile	Ile	Gly	Val	Val	Phe	Ile	Leu	Val	Leu
			180					185					190		
Ser	Leu	Phe	Leu	Gly	Val	Arg	Glu	Lys	Arg	Arg	Ile	Val	Arg	Glu	Leu
		195					200					205			
Gly	Ala	Leu	Pro	Ala	Val	Ala	Asp	Leu	Ile	Lys	Pro	Ala	Pro	Leu	Ser
	210					215						220			

Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Asn
 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu
 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
 405 410 415

Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly
 420 425 430

Ile Val Pro Leu Pro
 435

<210> 60
 <211> 1155
 <212> DNA
 <213> Neisseria gonorrhoeae

<220>
 <221> CDS
 <222> (1) .. (1152)

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 Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln
 1 5 10 15
 act tat ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 96

Thr	Tyr	Leu	Tyr	Gln	Lys	Pro	Lys	Leu	Phe	Lys	Gly	Ala	Val	Arg	Asn	
		20						25					30			
ctc	gaa	gcc	gca	tct	tgt	aaa	tat	atc	aac	gag	ata	tac	caa	cga	gca	144
Leu	Glu	Ala	Ala	Ser	Cys	Lys	Tyr	Ile	Asn	Glu	Ile	Tyr	Gln	Arg	Ala	
	35					40					45					
gac	cca	acc	gca	ccg	ctg	ttt	cat	ctg	cgt	aaa	aaa	ggc	gca	atc	gtt	192
Asp	Pro	Thr	Ala	Pro	Leu	Phe	His	Leu	Arg	Lys	Lys	Gly	Ala	Ile	Val	
	50				55					60						
cct	aaa	gaa	gaa	tac	gtc	gaa	agt	ttc	gac	gat	tgg	ggc	aaa	act	cgc	240
Pro	Lys	Glu	Glu	Tyr	Val	Glu	Ser	Phe	Asp	Asp	Leu	Gly	Lys	Thr	Arg	
	65			70					75					80		
tac	cgt	ttt	att	aaa	tcc	gtt	atc	tac	gaa	cat	atg	aag	aat	ggg	gcg	288
Tyr	Arg	Phe	Ile	Lys	Ser	Val	Ile	Tyr	Glu	His	Met	Lys	Asn	Gly	Ala	
		85						90					95			
tcg	tta	gtc	tat	aac	cat	att	aac	aac	gag	ccg	ttt	tca	gac	cat	atc	336
Ser	Leu	Val	Tyr	Asn	His	Ile	Asn	Asn	Glu	Pro	Phe	Ser	Asp	His	Ile	
	100						105					110				
gcc	cgt	caa	gtc	gcc	cgc	ttt	gcc	ggc	gca	cat	act	att	gtt	agt	gga	384
Ala	Arg	Gln	Val	Ala	Arg	Phe	Ala	Gly	Ala	His	Thr	Ile	Val	Ser	Gly	
	115						120					125				
tat	ctt	gct	ttt	ggc	agc	gac	gaa	tct	tat	aaa	aac	cat	tgg	gat	acc	432
Tyr	Leu	Ala	Phe	Gly	Ser	Asp	Glu	Ser	Tyr	Lys	Asn	His	Trp	Asp	Thr	
	130				135					140						
cgc	gat	gtg	tat	gcc	atc	cag	ctt	ttc	ggc	aag	aaa	cgt	tgg	caa	ctt	480
Arg	Asp	Val	Tyr	Ala	Ile	Gln	Leu	Phe	Gly	Lys	Lys	Arg	Trp	Gln	Leu	
	145				150				155				160			
act	gcc	cct	gat	ttc	cct	atg	cca	tgg	tat	atg	caa	cag	act	aaa	gat	528
Thr	Ala	Pro	Asp	Phe	Pro	Met	Pro	Leu	Tyr	Met	Gln	Gln	Thr	Lys	Asp	
		165						170					175			
act	gat	att	tcc	att	cct	gaa	cat	atc	gat	atg	gat	att	ctc	ctt	gaa	576
Thr	Asp	Ile	Ser	Ile	Pro	Glu	His	Ile	Asp	Met	Asp	Ile	Ile	Leu	Glu	
		180						185					190			
gca	ggt	gat	gtc	ctc	tac	atc	cca	cgc	ggt	tgg	tgg	cac	aga	cct	atc	624
Ala	Gly	Asp	Val	Leu	Tyr	Ile	Pro	Arg	Gly	Trp	Trp	His	Arg	Pro	Ile	
	195						200					205				
cgc	ctc	ggc	tgt	gaa	acc	ttc	cac	ttc	gct	gtc	ggg	acc	ttc	cca	cca	672
Pro	Leu	Gly	Cys	Glu	Thr	Phe	His	Phe	Ala	Val	Gly	Thr	Phe	Pro	Pro	
	210				215					220						
aac	ggc	tat	aat	tac	ctc	gag	tgg	cta	atg	aag	aaa	ttt	ccc	acc	ata	720
Asn	Gly	Tyr	Asn	Tyr	Leu	Glu	Trp	Leu	Met	Lys	Lys	Phe	Pro	Thr	Ile	
	225				230				235				240			
gaa	agt	ctg	cgc	cac	agt	ttc	tca	gac	tgg	gag	caa	gat	agg	acg	cgt	768
Glu	Ser	Leu	Arg	His	Ser	Phe	Ser	Asp	Trp	Glu	Gln	Asp	Arg	Thr	Arg	
		245						250					255			
atc	aac	gat	act	gcc	gca	caa	att	gct	gcc	atg	att	gcc	gac	ccc	gtc	816

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Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val
260 265 270
aat tat gaa gcc ttc agt gaa gac ttt ctc ggc aaa gaa cgt acc gat 864
Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp
275 280 285
acc gct ttt cat ctc gaa cag ttc ggc aat ccc aac gct act cgg ctt 912
Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu
290 295 300
tca gac gac gtc agg ttg aga tta aat gcc aat aat ttg gat acg ttg 960
Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu
305 310 315 320
gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gag 1008
Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu
325 330 335
ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa cgg tta ttg 1056
Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu
340 345 350
ttg aaa aat cta ctg gtt aac ttc aat cag gca aaa cat gaa gaa gtt 1104
Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val
355 360 365
agg aag ttg atc tac cag ttg ata gag tta gat ttt ctg gaa att ttg 1152
Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu
370 375 380
tga 1155

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<210> 61
 <211> 384
 <212> PRT
 <213> Neisseria gonorrhoeae

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<400> 61
Met Gly Ile His Leu Asp Phe Gly Ile Ser Pro Lys Thr Phe Arg Gln
1 5 10 15
Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
20 25 30
Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
35 40 45
Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
50 55 60
Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
65 70 75 80
Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
85 90 95
Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
100 105 110

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Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu
145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp
165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu
180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile
195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro
210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile
225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg
245 250 255

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val
260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp
275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu
290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu
305 310 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu
325 330 335

Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu
340 345 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val
355 360 365

Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu
370 375 380

<210> 62
<211> 717
<212> DNA
<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(714)

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atg aat aga ccc aag caa ccc ttc ttc cgt ccc gaa gtc gcc gtt gcc 48
Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala
1 5 10 15

cgc caa acc agc ctg acg ggt aaa gtg att ctg aca cga ccg ttg tca 96
Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser
20 25 30

ttt tcc cta tgg acg aca ttt gca tgg ata tct gcg tta ttg att atc 144
Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile
35 40 45

ctg ttt ttg ata ttt ggt aac tat acg cga aag aca aca gtg gag gga 192
Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly
50 55 60

caa att tta cct gca tgc gcc gta atc agg gtg tat gca ccg gat acg 240
Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
65 70 75 80

ggg aca att aca gcg aaa ttc gcg gaa gat gga gaa aag gtt aag gct 288
Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala
85 90 95

ggc gac aag cta ttt gcg ctt tgg aac tta cgt ttc ggc gca gga gat 336
Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
100 105 110

agc gtg cag cag cag ctg tgg aaa acg gag gca gtt ttg aag aaa acg ttg 384
Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
115 120 125

gca gaa cag gaa ctg ggt cgt ctg aag ctg ata cac ggg aat gaa acg 432
Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
130 135 140

cgc agc ctt aaa gca act gtc gaa cgt ttg gaa aac cag gaa ctc cat 480
Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Glu Leu His
145 150 155 160

att tgc caa cag ata gac ggt cag aaa agg cgc att aga ctt gcg gaa 528
Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
165 170 175

gaa atg ttg cag aaa tat cgt ttc cta tcc gcc aat gat gca gtc cca 576
Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
180 185 190

aaa caa gaa atg atg aat gtc aag gca gag ctt tta gag cag aaa gcc 624
Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala
195 200 205

aaa ctt gat gcc tac cgc cga gaa gaa gtc ggg ctg ctt cag gaa atc 672
Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
210 215 220

cgc acg cag aat ctg aca ttg gcc agc ctc ccc caa gcg gca tga 717
Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
225 230 235

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<210> 63

<211> 238

<212> PRT

<213> *Neisseria meningitidis*

<400> 63

Met Asn Arg Pro Lys Gln Pro Phe Phe Arg Pro Glu Val Ala Val Ala
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Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser
20 25 30

Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile
35 40 45

Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly
50 55 60

Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
65 70 75 80

Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala
85 90 95

Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
100 105 110

Ser Val Gln Gln Gln Leu Lys Thr Glu A'a Val Leu Lys Lys Thr Leu
115 120 125

Ala Glu Gln Gln Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
130 135 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Glu Leu His
145 150 155 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
180 185 190

Lys Glu Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala
195 200 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
210 215 220

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
225 230 235

<210> 64

<211> 690

<212> DNA

<213> *Neisseria meningitidis*

<220>

<222> (1) . . (687)

400> 64																									
atg atg aaat gtc gag gca gag ctt tta gag cag aaa gcc aaa ctt gat	48																								
Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp																									
1 5 10 15																									
gcc tac gcc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag	96																								
Ala Tyr Gly Arg Glu Glu Ala Glu Leu Leu Gln Glu Ile Arg Thr Gln																									
20 25 30																									
aac ctg aca ttg gcc agc ctc ccg aaa cgq cat gag aca gaa caa agc	144																								
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser																									
35 40 45																									
cag ctt gaa cgc acc atg gcc gat att cct caa gaa gtt ttg gat ttt	192																								
Gin Leu Glu Arg Thr Met Ala Asp ile Ser Gln Glu Val Leu Asp Phe																									
50 55 60																									
gaa atg cgc tct gaa caa atc atc cgt gra gga cgg tcg ggt tat ata	240																								
Glu Met Arg Ser Glu Gln ile ile Arg ala Gly Arg Ser Gly Tyr ile																									
65 70 75 80																									
gca ata ccg aac gtc gaa gtc gga cgg cag gtt gat cct tcc aaa ctg	288																								
Ala ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu																									
85 90 95																									
ctc ttg agc att gtt ccg gaa cgt acc gag tta tat gcc cat cta tat	336																								
Leu Leu Ser ile Val Pro Glu Arg Trp Glu Leu Tyr Ala His Leu Tyr																									
100 105 110																									
atc ccc agc agt gca gca ggc ttt atc aag ccg aaa gac aag gtt gtc	384																								
Ile Pro Ser Ser Ala Ala Gly Phe ile Lys Pro Lys Asp Lys Val Val																									
115 120 125																									
cta cgt tat cag gca tar ccc tat cag aaa ttc ggg ctt got tcc ggc	432																								
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly																									
130 135 140																									
agt gtc gta tca gtg gca aaa acg gcc ctg gcc aga cag gaa ttg tcg	480																								
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser																									
145 150 155 160																									
gga ttg gcc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt	528																								
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val																									
165 170 175																									
tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt	576																								
Tyr Leu Val Lys ile Lys Pro Asp Lys Pro Thr ile Thr Ala Tyr Gly																									
180 185 190																									
gag gaa aaa ccg ctg caa atc ggc atg acg ctg gaa gca gac atc cta	624																								
Glu Glu Lys Pro Leu Gln ile Gly Met Trp Leu Glu Ala Asp ile Leu																									
195 200 205																									
cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ccg att tac agt	672																								
His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro ile Tyr Ser																									
210 215 220																									
atg tcs gcc agg ttg taa	690																								
Met Ser Gly Arg Leu																									
225																									

<210> 65
 <211> 229
 <212> PRT
 <213> Neisseria gonorrhoeae

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<400> 65
Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp
 1             5             10             15

Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
                20             25             30

Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
 35             40             45

Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
 50             55             60

Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
 65             70             75             80

Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu
                85             90             95

Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
 100            105            110

Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
 115            120            125

Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
 130            135            140

Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
 145            150            155            160

Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
 165            170            175

Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
 180            185            190

Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
 195            200            205

His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser
 210            215            220

Met Ser Gly Arg Leu
 225
    
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<210> 66
 <211> 924
 <212> DNA
 <213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(921)

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<400> 66
atg caa tac agc aca ctg gca gga caa acc gac aac tcc ctc gtt tcc 48
Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser
1 5 10 15

aat aat ttc ggg ttt ttg cgc ctg cgc ctt aat ttt atg cgc tat gaa 96
Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
20 25 30

agc cat gcc gat tgg gtt att acc ggc gtg cct tat gat atg cgc gtt 144
Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
35 40 45

tca ggg cgt tcc ggc gcg cgt ttc ggt cct gaa gcc atc cgg cgc gcc 192
Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
50 55 60

tcc gtc aac ctc gct tgg gag cac cgc agg ttt cgc tgg aca ttt gat 240
Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
65 70 75 80

gtg cgc gaa cgc ctg aac att att gat tgc gcc gac tgg gtt ttt tct 288
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
85 90 95

ttt ggc gac agc agg gat ttt gtc gaa aaa atg gaa gcg cac gcc gcc 336
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
100 105 110

aaa tta ctt tct ttc gcc aaa cgc tgt ttg agt ttg gcc gcc gac cat 384
Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
115 120 125

ttc att acc ctc cgc ttg ttg cgc gcc cac gcc cgc tat ttc gcc aaa 432
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
130 135 140

ctc gca ctg att cat ttt gac gcg cac acc gac acc tac gac aac gcc 480
Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
145 150 155 160

agc gaa tac gac cac gcc acg atg ttt tat acc gcc ccc aag gaa gcc 528
Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
165 170 175

ctc atc gac cgc tcc cgt tcc gta caa atc gcc ata cgc acc gaa cac 576
Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
180 185 190

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agt aaa aaa ttg cct ttt act gtg ttg tcc gcc ccc aaa gtc aat gaa 624
 Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
 195 200 205
 gac agt gtt gaa gag acc gtc cgt aaa atc aaa gaa acc gtc ggc aat 672
 Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
 210 215 220
 atg ccc gtt tac ctg act ttc gac ata gac tgt ctc gac ccg tcg ttc 720
 Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
 225 230 235 240
 gcc ccc ggg acc ggt acg ccc gta tgc ggc ggc ttg agc agc gac agg 768
 Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
 245 250 255
 gca tta aaa atc cta cgt ggg ctg acg gat ctc gac atc gtc ggt atg 816
 Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
 260 265 270
 gat gtt gta gaa gtt gcc ccc tct tac gac caa tcc gac att acc gct 864
 Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
 275 280 285
 ttg gcc ggc gtc aca att gcc ttg gaa atg ctt tac ctt caa ggt ggc 912
 Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
 290 295 300
 aaa aag gac tga 924
 Lys Lys Asp
 305

<210> 67
 <211> 307
 <212> PRT
 <213> Neisseria gonorrhoeae

<400> 67
 Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser
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 Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
 20 25 30
 Ser His Ala Asp Trp Val Ile Thr Glu Val Pro Tyr Asp Met Ala Val
 35 40 45
 Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
 50 55 60
 Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
 65 70 75 80
 Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
 85 90 95
 Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
 100 105 110

Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
245 250 255

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Cln Gly Ala
290 295 300

Lys Lys Asp
305

<210> 68
<211> 1404
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(1401)

<400> 68
atg aca ttg ctg aac cta atg ata atg caa gat tac ggt att tcc gtt 48
Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
1 5 10 15

tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tgg gct atg 96
Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
20 25 30

aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144

Lys	Ser	Tyr	Phe	Ser	Lys	Tyr	Ile	Leu	Pro	Val	Ser	Leu	Phe	Thr	Leu	
35						40						45				
cca	cta	tcc	ctt	tcc	cca	tcc	ggt	tgg	gct	ttt	acg	ctg	cct	gaa	gca	192
Pro	Leu	Ser	Leu	Ser	Pro	Ser	Val	Ser	Ala	Phe	Thr	Leu	Pro	Glu	Ala	
50						55						60				
tgg	cgg	gcg	gcg	cag	caa	cat	tgg	gct	gat	ttt	caa	gcg	tcc	cat	tac	240
Trp	Arg	Ala	Ala	Gln	Gln	His	Ser	Ala	Asp	Phe	Gln	Ala	Ser	His	Tyr	
65						70						75				
cag	cgt	gat	gca	gtg	cgc	gca	cgg	caa	caa	gcc	aag	gcc	gca	ttc		288
Gln	Arg	Asp	Ala	Val	Arg	Ala	Arg	Gln	Gln	Gln	Ala	Lys	Ala	Ala	Phe	
85						90						95				
ctt	ccc	cat	gta	tcc	gcc	aat	gcc	agc	tac	cag	cgc	cag	ccg	cca	tgg	336
Leu	Pro	His	Val	Ser	Ala	Asn	Ala	Ser	Tyr	Gln	Arg	Gln	Pro	Pro	Ser	
100						105						110				
att	tct	tcc	acc	cgc	gaa	aca	cag	gga	tgg	agc	gtg	cag	gtg	gga	caa	384
Ile	Ser	Ser	Thr	Arg	Glu	Thr	Gln	Gly	Trp	Ser	Val	Gln	Val	Gly	Gln	
115						120						125				
acc	tta	ttt	gac	gct	gcc	aaa	ttt	gca	caa	tac	cgc	caa	agc	agg	ttc	432
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Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp	
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Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val	
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Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp	
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Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu	
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Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp	
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<212> PRT
<213> Neisseria meningitidis
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 Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
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 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
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 Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80
 Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95
 Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110
 Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
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 Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
 130 135 140
 Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
 145 150 155 160
 Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
 165 170 175
 Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
 180 185 190
 Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
 195 200 205
 Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
 210 215 220
 Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
 225 230 235 240
 Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
 245 250 255
 Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
 260 265 270
 Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
 275 280 285
 Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
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 Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
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Thr	Leu	Gly	Ile	Cys	Ala	Leu	Leu	Ala	Phe	Cys	Phe	Gly	Ala	Ala	Ile			
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Ala	Ser	Gly	Tyr	His	Leu	Glu	Tyr	Glu	Tyr	Gly	Tyr	Arg	Tyr	Ser	Ala			
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gtg	ggc	gct	tgg	gct	gtt	gtt	tta	tta	tta	tgt	gca	cgc	ggc				192	
Val	Gly	Ala	Leu	Ala	Ser	Val	Val	Phe	Leu	Leu	Leu	Leu	Ala	Arg	Gly			
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tcc	cgg	cgc	gtt	tct	tca	ggt	gtt	tta	ctg	att	tac	gtc	ggc	aca	acc		240	
Phe	Pro	Arg	Val	Ser	Ser	Val	Val	Leu	Leu	Ile	Tyr	Val	Gly	Thr	Thr			
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Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
85 90 95

ata gtc ggt tgc ata ttg gaa agc aat cct gcc gag gcg cgt gaa ttt 336
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
100 105 110

gtc ggc aat ctc ccc ggg tgc ctt tat ttt gtg cag gca tta ttt ttc 384
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
115 120 125

att ttt ggc ttg aca gtt tgg aaa tat tgt gta tct gtg ggg gta ttt 432
Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe
130 135 140

gct gac gta aaa aac tat aaa cgt cgc agc aaa ata tgg ctg acc ata 480
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
145 150 155 160

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Leu Leu Thr Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly
165 170 175

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Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
180 185 190

gac ctg tat tac gac ttg gct ttc cgc gcc ggc aca ata tgc cgc caa 624
Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln
195 200 205

gcg cgc cca cat ttt gga agc agc aaa asa agc gtc aac atg gca tat 672
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ccg cca act tgc gtc caa gta taa 696
Pro Pro Thr Cys Ala Gln Val
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<213> Neisseria gonorrhoeae

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Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
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Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr

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Ala	Gly	Leu	Arg	Asp	Ala	Ile	Ala	Glu	Lys	Gly	Gly	Asp	Pro	Ala	Lys	
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Val	Glu	Cys	Gly	Gly	Tyr	Asp	Pro	Asp	Ala	Phe	Arg	Lys	Asn	Arg	Glu	
		130				135					140					
atc	gaa	gac	aga	cgt	aac	gaa	gac	cgt	ttc	cac	ttc	atc	aac	tgg	aca	480
Ile	Glu	Asp	Arg	Arg	Asn	Glu	Asp	Arg	Phe	His	Phe	Ile	Asn	Trp	Thr	
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aaa	acc	gct	ttt	gaa	aat	gtg	gac	gtg	att	ccg	gcg	ggc	aac	ggc	atc	528
Lys	Thr	Ala	Phe	Glu	Asn	Val	Asp	Val	Ile	Pro	Ala	Gly	Asn	Gly	Ile	
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Met	His	Gln	Ile	Asn	Leu	Glu	Lys	Met	Ser	Pro	Val	Val	Gln	Val	Lys	
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Asn	Gly	Val	Ala	Phe	Pro	Asp	Thr	Cys	Val	Gly	Thr	Asp	Ser	His	Thr	
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Pro	His	Val	Asp	Ala	Leu	Gly	Val	Ile	Ser	Val	Gly	Val	Gly	Gly	Leu	
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gaa	gtc	gaa	acc	gta	atc	ctg	gga	cgc	gcg	tcc	atc	acg	cgc	ctg	ccc	720
Glu	Glu	Glu	Thr	Val	Met	Leu	Gly	Arg	Ala	Ser	Met	Met	Arg	Leu	Pro	
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Asp	Ile	Val	Gly	Val	Glu	Lys	Asn	Gly	Lys	Arg	Lys	Ala	Gly	Ile	Thr	
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gcg	acg	gat	att	ctg	ctg	gca	ctg	acc	gag	ttt	ctg	cgc	aaa	gaa	cgc	816
Ala	Thr	Asp	Ile	Val	Leu	Ala	Leu	Thr	Glu	Phe	Leu	Arg	Lys	Glu	Arg	
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ggc ccg agc aac ccg cac gcg cgt ttt gcg acc gcc gat ttg gcc gcc Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly 370 375 380	1152
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tgt aac gcc atg agc gcc gcg ctg gat ccg aaa atc cag aaa gaa atc Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile 485 490 495	1488
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1728	aaa gac att tgg cct acc gat gaa gaa atc gat gcc atc gtt gcc gaa	
	Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu	575
1776	tat gtg aaa ccg cag caa ttt cgc gac gtt tat atc ccg atg ttc gac	
	Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp	590
1824	acc ggc aca gcg caa aaa gca cca agc ccg ctg tac gac tgg cgt cca	
	Thr Gly Thr Ala Gln Leu Ala Pro Ser Pro Leu Tyr Tyr Asp Trp Phe Pro	605
1872	atg tct acc acc tat atc cgc cgc cca cct tac tgg gaa ggc gca ctg gca	
	Met Ser Thr Thr Thr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala	620
1920	ggg gaa cgc aca tta agc ggt atg cgt ccg ctg gcg atg ttt tgg ccc gac	
	Gly Gly Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp	635
1968	aac atc acc acc gac cat ctc ctg cca tcc aat gcg att ttg gca agc	
	Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala Ser	650
2016	agt gcc gca ggc gaa tat ttg gca aaa atg ggt ttg cct gaa gaa gac	
	Ser Ala Ala Gly Gly Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp	665
2064	ttc aac tct tac gca acc cac cgt ggc gac cac ttg acc gcc caa cgc	
	Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg	680
2112	gca acc ttc gcc aat ccg aaa ctg ttt aac gaa atg gtg aga aac gaa	
	Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu	695
2160	gac ggc agc gta cgc caa ggt tgc ctg gca cgc gtt gaa ccc gaa ggc	
	Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Asp Val Glu Pro Glu Gly	710
2208	caa acc atc cgc atg tgg gaa gcc atc gaa acc tat atg aac cgc aaa	
	Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys	725
2256	cgn ccg ctc atc atc att gcc ggc gcg gac tac ggt caa ggc tca agc	
	Gln Thr Thr Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser	740
2304	cgc sac tgg gct gca aaa ggc gta cgc ctc gcc gtc gtg gaa cgc att	
	Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile	755
2352	gtt gcc gaa ggc ttc gac cgt atc cac cgc acc aac tct atc ggt atg	
	Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met	770

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caa ctg gac ggt acg gaa acc tac gac gtt gtc ggc gaa cgc aca ccg 2448
Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro
805 810 815

cgc tgc gac ctg acc ctt gtg att cac cgt aaa aac ggc gag acc gtc 2496
Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val
820 825 830

gaa gtc ccc att acc tgc cgc ctc gat acc gca gaa gaa gtg ttg gta 2544
Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val
835 840 845

tat gaa gcc ggt ggc gta ttg caa cgg ttt gca cag gat ttt ttg gaa 2592
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Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
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Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
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Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
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Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
100 105 110

Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala
115 120 125

Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu
130 135 140

Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr
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Lys	Leu	Thr	Gly	Arg	Asp	Asp	Ala	Gln	Val	Lys	Leu	Val	Glu	Thr	Tyr
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Pro	Arg	Val	Leu	Lys	Phe	Asp	Leu	Ser	Ser	Val	Thr	Arg	Asn	Met	Ala
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Gly	Pro	Ser	Asn	Pro	His	Ala	Arg	Phe	Ala	Thr	Ala	Asp	Leu	Ala	Gly
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Arg	Leu	Gly	Leu	Gln	Arg	Lys	Pro	Trp	Val	Lys	Ser	Ser	Phe	Ala	Pro
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Pro	Pro	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Ser	Ile	Arg	Phe	Asp
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Lys	Asp	Ile	Trp	Pro	Thr	Asp	Glu	Glu	Ile	Asp	Ala	Ile	Val	Ala	Glu
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Met	Ser	Thr	Tyr	Ile	Arg	Arg	Pro	Pro	Tyr	Trp	Glu	Gly	Ala	Leu	Ala
		610				615					620				
Gly	Glu	Arg	Thr	Leu	Ser	Gly	Met	Arg	Pro	Leu	Ala	Ile	Leu	Pro	Asp
625				630						635					640
Asn	Ile	Thr	Thr	Asp	His	Leu	Ser	Pro	Ser	Asn	Ala	Ile	Leu	Ala	Ser
			645						650					655	
Ser	Ala	Ala	Gly	Glu	Tyr	Leu	Ala	Lys	Met	Gly	Leu	Pro	Glu	Glu	Asp
		660						665					670		
Phe	Asn	Ser	Tyr	Ala	Thr	His	Arg	Gly	Asp	His	Leu	Thr	Ala	Gln	Arg
		675					680				685				
Ala	Thr	Phe	Ala	Asn	Pro	Lys	Leu	Phe	Asn	Glu	Met	Val	Arg	Asn	Glu
		690				695					700				
Asp	Gly	Ser	Val	Arg	Gln	Gly	Ser	Leu	Ala	Arg	Val	Glu	Pro	Glu	Gly
705				710						715					720
Gln	Thr	Met	Arg	Met	Trp	Glu	Ala	Ile	Glu	Thr	Tyr	Met	Asn	Arg	Lys
			725						730					735	
Gln	Pro	Leu	Ile	Ile	Ile	Ala	Gly	Ala	Asp	Tyr	Gly	Gln	Gly	Ser	Ser
		740						745					750		
Arg	Asp	Trp	Ala	Ala	Lys	Gly	Val	Arg	Leu	Ala	Gly	Val	Glu	Ala	Ile
		755					760					765			
Val	Ala	Glu	Gly	Phe	Glu	Arg	Ile	His	Arg	Thr	Asn	Leu	Ile	Gly	Met
		770				775					780				
Gly	Val	Leu	Pro	Leu	Gln	Phe	Lys	Pro	Gly	Thr	Asn	Arg	His	Thr	Leu
785				790						795					800

Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro
805 810 815

Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val
820 825 830

Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val
835 840 845

Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu
850 855 860

Gly Asn Ala Ala
865

<210> 74
<211> 1170
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(1167)

<400> 74
atg cag caa att aaa att ccc gcc gtt tac tac cgt ggc ggt aca tca 46
Met Pro Gln Ile Lys Ile Pro Ala Val Tyr Tyr Arg Gly Gly Thr Ser
1 5 10 15

aaa ggc gtg ttt ttc aaa cgt tcc gac ctg ccc gag gcg gcg cgg gaa 96
Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
20 25 30

gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg 144
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
35 40 45

gat ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agc tcg tcc 192
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 55 60

acc agc aag gcg gtg att ttg gac aag tcc gaa cgc gcc gat cac gat 240
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp
65 70 75 80

gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
85 90 95

tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110

atc gag caa ggc ttg gtc gat aaa ggc aag att cct tca gac gcc atc 384
Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile
115 120 125

cat Cys	gta Thr	ccg Val	atg Lys	caa Ile	aac Trp	ggc Gln	gca Lys	gtt Asn	ttg Ile	gaa Gly	aca Lys	acc Thr	att Ile	att Ile	gcc Ala	432
130						135				140						
cat His	gta Val	ccg Pro	atg Met	caa Gln	aac Asn	ggc Gly	gca Ala	gtt Val	ttg Leu	gaa Glu	aca Thr	ggc Gly	gat Asp	ttt Phe	gag Glu	480
145					150					155					160	
ctc Leu	gac Asp	ggc Gly	gta Val	acg Thr	ttc Phe	ccg Pro	gca Ala	gcc Ala	gaa Glu	gta Val	caa Gln	atc Ile	gaa Glu	ttt Phe	ctt Leu	528
				165					170					175		
gat Asp	cca Pro	gcc Ala	gac Asp	ggc Gly	gaa Glu	ggc Gly	agt Ser	atg Met	ttc Phe	cca Pro	acc Thr	ggc Gly	aat Asn	ttg Leu	gtc Val	576
				180				185					190			
gat Asp	gaa Glu	att Ile	gat Asp	gtg Val	ccg Pro	aat Asn	ata Ile	ggc Gly	cgt Arg	ttg Leu	aaa Lys	gcc Ala	acg Thr	ctc Leu	atc Ile	624
		195					200					205				
aac Asn	gcg Ala	ggc Gly	att Ile	ccg Pro	acc Thr	gtt Thr	ttc Phe	ctg Leu	aat Asn	gcc Ala	gcc Ala	gac Asp	ttg Leu	ggc Gly	tac Tyr	672
		210				215						220				
acg Thr	ggc Gly	aaa Lys	gag Glu	ttg Leu	caa Gln	gac Asp	gac Asp	atc Ile	aac Asn	aac Asn	gat Asp	gcc Ala	gca Ala	gct Ala	ttg Leu	720
	225				230					235					240	
gaa Glu	aaa Lys	ttc Phe	gag Glu	aaa Lys	atc Ile	cgc Arg	gct Ala	tac Tyr	ggc Gly	ctg Ala	aaa Leu	atg Lys	ggc Met	ctg Gly	ctg Leu	768
				245					250				255			
atc Ile	agc Ser	gac Asp	gta Val	tcc Ser	gaa Glu	gct Ala	gcc Ala	gcc Ala	cgc Arg	gcg Ala	cac His	acg Thr	ccg Pro	aaa Lys	gtc Val	816
			260					265					270			
gcc Ala	ttc Phe	gtc Val	gcg Ala	ccc Pro	gcc Ala	gcc Ala	gat Ala	tac Asp	acc Tyr	gcc Thr	tcc Ala	agt Ser	ggc Ser	aaa Gly	acc Thr	864
			275				280					285				
gtg Val	aat Asn	gcc Ala	gcc Ala	gac Asp	atc Ile	gat Asp	ttg Leu	ctg Leu	gta Val	cgc Arg	gcc Ala	ctg Ala	agc Ser	atg Met	ggc Gly	912
	290					295					300					
aaa Lys	ttg Leu	cac His	cac His	gcg Ala	atg Met	atg Met	ggc Gly	acc Thr	gcc Ala	tct Val	gtt Ser	gcc Val	att Ala	gcg Ile	acc Thr	960
	305				310					315				320		
gcc Ala	gcc Ala	gcc Ala	gtg Val	ccc Pro	ggc Gly	acg Thr	ctg Leu	gtc Val	aac Asn	ctt Leu	gcc Ala	ggc Ala	ggc Gly	ggc Gly	gga Gly	1008
				325					330					335		
acg Thr	cgt Arg	aaa Lys	gaa Glu	gtg Val	gcg Arg	ttc Phe	ggg Gly	cat His	cct Pro	tcc Ser	ggc Gly	aca Thr	ttg Leu	cgc Arg	gtc Val	1056
				340				345					350			
ggc Gly	gca Ala	gcc Ala	gcc Ala	gaa Glu	tgt Cys	cag Gln	gac Asp	gga Gly	caa Gln	tgg Trp	acg Thr	gcc Ala	acc Thr	aaa Lys	gcg Ala	1104
				355			360					365				
gtt Val	atg Met	agc Ser	cgc Arg	agc Ser	gca Ala	cgc Arg	gtg Val	atg Met	atg Met	gaa						

400> 75																
Met	Pro	Gln	Ile	Lys	Ile	Pro	Ala	Val	Tyr	Tyr	Arg	Gly	Gly	Thr	Ser	
1				5					10					15		
Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu																
			20					25					30			
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro																
			35				40					45				
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser																
			50				55					60				
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp																
			65			70				75					80	
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp																
				85					90						95	
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala																
			100						105					110		
Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile																
			115				120					125				
Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala																
			130				135				140					
His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu																
			145			150				155					160	
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu																
				165					170					175		
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val																
				180					185					190		
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile																
			195				200					205				
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr																
			210				215					220				
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Leu																
			225			230				235						240

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
245 250 255

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
260 265 270

Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
275 280 285

Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
290 295 300

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
305 310 315 320

Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly
325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
340 345 350

Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
355 360 365

Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
370 375 380

Pro Glu Asp Cys Phe
385

<210> 76

<211> 2094

<212> DNA

<213> Neisseria gonorrhoeae

<220>

<221> CDS

<222> (1)..(2091)

<400> 76
atg aat tgc acc gca agt aaa acc ctg aaa gga ttg tgc ctg gtg ttt 48
Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe
1 5 10 15

ttc gcc tct ggc ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
20 25 30

ctt cta ttc agc cac ata ggt atc gat ttg agt tgc att act gtc att 144
Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
35 40 45

att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggc gga 192
Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
50 55 60

ggc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc 240
Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile

65	70										75	80									
gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc aag ggt ctg att																					
Ala Glu Val Ser Ile	85										90	95									
gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc aag ggt ctg att																					
Ala Glu Val Ser Ile	85										90	95									
tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct																					
Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala	100										105	110									
tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct																					
Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala	100										105	110									
gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc gcg																					
Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala	115										120	125									
acc ttg ccc ttg ctg acc tgt ttt ttt aac cgg aaa ata cat aat gtt																					
Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val	130										135	140									
gcg gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca																					
Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala	145										150	155									
ctc gga tgc ctt gcc gcc gcc gaa ttt ttc tac gtc ttt ttt acc ctc																					
Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu	165										170	175									
tcc caa acc att gcc ctg acc gcc tgc ctt aac ctt ctg att gct gct																					
Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala	180										185	190									

305	310	315	320	
ggg ttg att ttc cca ctt gta cac cat gtg ggt acg gat ggc aac aaa				1008
Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys				
325	330	335		
tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt				1056
Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser				
340	345	350		
gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttg ttg tcc				1104
Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser				
355	360	365		
acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct				1152
Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro				
370	375	380		
ttg ttt tgt aca ctg ttc caa aaa agt ctc cga ctg aat gca gtg tcg				1200
Val Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser				
385	390	395	400	
gta gca gtt tcc cta atg ttc ggc atc ctc atg ttc cta ctg ccg gat				1248
Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp				
405	410	415		
tct gtc ttt caa aat att gct ggc cgt ccg gat agg ttg att gaa aac				1296
Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn				
420	425	430		
aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt				1344
Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val				
435	440	445		
tat ggg gcg aat gta tac gac ggc gca tac aat acc gat ata ttc aat				1392
Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn				
450	455	460		
agt gtc aac ggc atc gaa cgt gcc tat ctg cta ccc tcc ctg aag tcc				1440
Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser				
465	470	475	480	
ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tcg tgg gcg				1488
Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala				
485	490	495		
cgc gtc ttg tct gcc att ccg gaa atg cag tcg atg atc gtt gcg gaa				1536
Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu				
500	505	510		
atc aat ccg gca tac cgt agc ctt atc gcg gac gag ccg caa atc gca				1584
Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala				
515	520	525		
cgc ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg				1632
Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg				
530	535	540		
aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg				1680
Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met				

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<210> 77
<211> 697
<212> PRT
<213> Neisseria gonorrhoeae
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400> 77
Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe
1      5      10      15
Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
      20      25      30
Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
      35      40      45
Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
      50      55      60
Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
      65      70      75      80

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Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile
85 90 95

Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala
100 105 110

Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala
115 120 125

Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
130 135 140

Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala
145 150 155 160

Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu
165 170 175

Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala
180 185 190

Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro
195 200 205

Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser
210 215 220

Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln
225 230 235 240

Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly
245 250 255

Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe
260 265 270

Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala
275 280 285

Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly
290 295 300

Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg
305 310 315 320

Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys
325 330 335

Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser
340 345 350

Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser
355 360 365

Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro
370 375 380

Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser
385 390 395 400

Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp
405 410 415

Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn
420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val
435 440 445

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn
450 455 460

Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser
465 470 475 480

Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala
485 490 495

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu
500 505 510

Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala
515 520 525

Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
530 535 540

Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
545 550 555 560

Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
595 600 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
610 615 620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Lys Gln Arg Leu Ser
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
645 650 655

Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met
660 665 670

Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile
675 680 685

Val Glu Tyr Lys Tyr Gly Arg Gly Ile
690 695

- <210> 78
<211> 39
<212> DNA
<213> Artificial sequence

<223> Artificial sequence description: PCR primer

gctctagacc accatgtctg aagaaaaaatt gaaaatgag 39

<211> 32

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

cgggatccag aaatggctgg attcgctatc ag 32

<211> 32

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

gctctagacc accatgaaac acttactcat cg 32

<211> 27

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

cgggatccaa tacgtaggac ttgggtc 27

<210> 82
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: PCR primer

<400> 82
gctctagacc accatgaaaa aatccctttt cgttc 35

<210> 83
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: PCR primer

<400> 83
cgggatccat tgcggataaa catattccgc c 31

<210> 84
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: PCR primer

<400> 84
gctctagacc accatgcgaa cgaccccaac cttc 34

<210> 85
<211> 30
<212> DNA
<213> Artificial sequence

<223> Artificial sequence description: PCR primer

cgggatccag aaccggtagc ctacgccgac 30

<211> 36

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

gctctagacc accatgaaca cacgcatcat cgtttc 36

<211> 30

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

cgggatccag caacggcctg cgcctttaag 30

<211> 34

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

gctctagacc accatgctga cgtttatcgg actg 34

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<210>      89
<211>      27
<212>      DNA
<213>      Artificial sequence

<220>
<223>      Artificial sequence description: PCR primer

<400>      89
cgggatccac ggcagaggca cgattcc                               27

<210>      90
<211>      34
<212>      DNA
<213>      Artificial sequence

<220>
<223>      Artificial sequence description: PCR primer

<400>      90
gctctagacc accatgggca tccatctcga cttc                       34

<210>      91
<211>      33
<212>      DNA
<213>      Artificial sequence

<220>
<223>      Artificial sequence description: PCR primer

<400>      91
cgggatccac aaaagttcca gaaaatctaa ctc                         33

<210>      92
<211>      33
<212>      DNA
<213>      Artificial sequence

<220>

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<223> Artificial sequence description: PCR primer

<400> 92

gctctagacc accatgaata gacccaagca acc 33

<210> 93

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 93

cgggatccat gccgcttggg ggagggc 26

<210> 94

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 94

gctctagacc accatgatga atgtcgagggc agag 34

<210> 95

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 95

cgggatccac agtttgcccg acatac 26

<210> 96

<212> DNA

<223> Artificial sequence description: PCR primer

gctctagacc accatgaaat tttttcctgc tcc 33

<211> 62

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

gaagatctag aaactgtaat tcaagttgaa ggaagatcta gaaactgtaa ttcaagttga 60

62 aq

<211> 33

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

gctctagacc accatgattg aatttgccg agc 33

<211> 54

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 99

ogggatccaa cctgogaag agttgoggg gatccaacc tgcagcaggt tgcg 54

<210> 100

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 100

gctctagacc accatgcaat acagcacact ggc 33

<210> 101

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 101

cgggatccag tcctttttcg caccttgaag 30

<210> 102

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: PCR primer

<400> 102

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<211> 30
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<210> 108

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<400> 108
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<210> 109

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<212> DNA

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<210> 113
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<210> 114
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<210> 115
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<210> 116
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<220>
<223> Artificial sequence description: PCR primer

<400> 116
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<210> 117
<211> 29
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<400> 117

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<211> 36

<212> DNA

<213> Artificial sequence

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<223> Artificial sequence description: PCR primer

<400> 118

ggactagtc accatggctg ccaaccaacg ttaccg 36

<210> 119

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<400> 119

qaaqatctaa gccgcgttcc cttccaaaaa atc 33

<210> 120

<211> 34

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<223> Artificial sequence description: PCR primer

<400> 120

gctctagacc accatgccgc aaattaaaat tccc 34

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cgggatccat tgggcaacga cgaaggcac 29

<210> 124

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09830723-09164

<220>

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<400> 124

gctctagacc accatgagaa tagagatcac acc 33

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<400> 127

cgggatccaa cctgcttcat gggtgattc 29

<211> 36

<213> Artificial sequence

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gctctagacc accatgaatt cgaccgcaag taaaac 36

<211> 28

<213> Artificial sequence

<223> Artificial sequence description: PCR primer

cgggatccaa atccctctgc cgtatttg 28